Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1542	1klo		920	1096	2.4e-20	0.36	0.13		CHAIN: A;	FAMILY
1542	1pfx	L	907	1065	3.6e-18	0.16	-0.03		LAMININ; CHAIN: NULL; FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	GLYCOPROTEIN GLYCOPROTEIN COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1542	1pfx	L	971	1112	4.8e-16	0.07	0.12		FACTOR IXA; CHAIN: C, L;; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN
1542	1qfk	L	915	1057	6e-22	0.05	-0.17		COAGULATION FACTOR VIIA (LIGHT CHAIN); CHAIN: L; COAGULATION FACTOR VIIA (HEAVY CHAIN); CHAIN: H; TRIPEPTIDYL INHIBITOR; CHAIN: C;	SERINE PROTEASE FVIIA; FVIIA; BLOOD COAGULATION, SERINE PROTEASE
1542	1tpg		907	949	6e-13	1.38	0.89		T-PLASMINOGEN ACTIVATOR F1-G; 1TPG 7 CHAIN: NULL; 1TPG 8	PLASMINOGEN ACTIVATION
1542	1vap	A	913	1050	6e-26	0.16	-0.18		PHOSPHOLIPASE A2; CHAIN: A, B;	LIPID DEGRADATION PHOSPHOLIPASE A2, LIPID DEGRADATION, HYDROLASE
1542	1whe		913	949	2.4e-13	0.51	0.72		COAGULATION FACTOR X; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN, HYDROLASE, SERINE PROTEASE, PLASMA, BLOOD 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1542	1xka	L	915	1065	4.8e-21	0.08	-0.08		BLOOD COAGULATION FACTOR XA; CHAIN: L, C;	BLOOD COAGULATION FACTOR STUART FACTOR; BLOOD COAGULATION FACTOR, SERINE PROTEINASE, EPIDERMAL 2 GROWTH FACTOR LIKE DOMAIN
1543	1b0w	A	1	95	2.8e-57			114.58	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
1543	1b0w	A	23	130	1.1e-66			129.17	BENCE-JONES KAPPA I PROTEIN BRE; CHAIN: A, B, C;	IMMUNE SYSTEM BENCE-JONES; IMMUNOGLOBULIN, AMYLOID, IMMUNE SYSTEM
1543	1b2w	L	23	176	2.8e-68			110.03	ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
1543	1b6d	A	23	145	9.8e-72	0.83	1.00		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1543	1bj1	J	23	145	2.8e-73	0.78	1.00		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1543	1bvk	A	1	95	1.4e-56			116.50	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1543	1bvk	A	23	130	5.6e-67			131.09	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1543	1bww	A	1	95	2.8e-59			118.29	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
1543	1bww	A	21	129	1.4e-66			130.32	IG KAPPA CHAIN V-I REGION REI; CHAIN: A, B;	IMMUNE SYSTEM REIV, STABILIZED IMMUNOGLOBULIN FRAGMENT, BENCE-JONES 2 PROTEIN, IMMUNE SYSTEM
1543	1ce1	L	23	145	2.8e-70	0.66	1.00		CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1543	1ce1	L	23	176	2.8e-70			112.27	CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1543	1dee	A	23	145	1.4e-74	0.73	1.00		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1543	1dfb	L	23	145	2.8e-69	0.78	1.00		CHAIN: G, H; IMMUNOGLOBULIN 3D6 FAB 1DFB 3	FAB VH3 3 SPECIFICITY
1543	1dql	L	1	95	7e-58			114.49	IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
1543	1dql	L	23	129	4.2e-65			128.96	IGM MEZ IMMUNOGLOBULIN; CHAIN: L; IGM MEZ IMMUNOGLOBULIN; CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN FOLD, ANTIBODY, IGM, FV
1543	1fgv	L	1	93	4.2e-60			118.13	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1543	1fgv	L	23	129	4.2e-69	0.88	1.00		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1543	1fgv	L	23	130	4.2e-69			131.11	IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1543	1fvc	A	1	95	2.8e-58			119.03	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									4D5, VERSION 8 1FVC 3	
1543	1fvc	A	23	131	2.8e-68			134.67	IMMUNOGLOBULIN FV FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 8 1FVC 3	
1543	1fvd	A	23	145	4.2e-71	0.73	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1543	1fvd	A	23	176	4.2e-71			112.07	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1543	1igm	L	1	93	1.3e-58			113.94	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
1543	1igm	L	23	137	2.8e-69	0.72	1.00		IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
1543	1igm	L	23	137	2.8e-69			132.78	IMMUNOGLOBULIN IMMUNOGLOBULIN M (IG-M) FV FRAGMENT 1IGM 3	
1543	1nmb	L	23	131	9.8e-59			122.77	N9 NEURAMINIDASE; 1NMB 4 CHAIN: N; 1NMB 5 FAB NC10; 1NMB 9 CHAIN: L, H; 1NMB 10	COMPLEX (HYDROLASE/IMMUNOGLOBULIN)
1543	1vge	L	23	145	2.8e-69	0.70	1.00		TR1.9 FAB; CHAIN: L, H;	IMMUNOGLOBULIN TR1.9, ANTI-THYROID PEROXIDASE, AUTOANTIBODY, 2 IMMUNOGLOBULIN
1543	1wtl	A	1	93	5.6e-57			117.28	IMMUNOGLOBULIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	FMF score	SEQFOLD score	Compound	PDB annotation
									WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
1543	1wtl	A	23	130	2.8e-66			131.61	IMMUNOGLOBULIN WAT, A VARIABLE DOMAIN FROM IMMUNOGLOBULIN LIGHT-CHAIN 1WTL 3 (BENCE-JONES PROTEIN) 1WTL 4	
1543	2fgw	L	23	145	1.3e-73	0.80	1.00		IMMUNOGLOBULIN FAB FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
1545	1cun	A	621	803	3.6e-06	-0.08	0.51		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN
1545	1hci	A	621	803	2.4e-07	-0.18	0.09		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
1545	1quu	A	621	803	1.2e-08	-0.43	0.24		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1546	1a4y	A	134	363	1.2e-25	0.10	1.00		RIBONUCLEASE	COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	(INHIBITOR/NUCLEASE) COMPLEX
										(INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1546	1a9n	A	113	213	2.8e-09	0.45	0.93		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
1546	1a9n	A	122	237	3.6e-17	0.13	0.66		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
1546	1a9n	A	136	265	4.8e-20	0.54	0.96		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
1546	1a9n	A	158	259	1.3e-08	0.12	0.47		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
1546	1a9n	A	206	343	1.1e-17	0.69	0.48		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
1546	1a9n	A	255	361	4.8e-17	0.22	0.33		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX
1546	1a9n	C	113	213	2.8e-09	0.17	0.89		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B";	(NUCLEAR PROTEIN/RNA), RNA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1546	1a9n	C	136	265	2.4e-19	0.74	0.83		CHAIN: B, D; U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1546	1a9n	C	158	259	1.3e-08	0.09	0.57		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1546	1a9n	C	206	343	8.4e-18	0.66	0.58		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1546	1a9n	C	255	383	6e-17	0.43	0.87		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1546	1d0b	A	128	329	2.4e-27	0.44	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1546	1d0b	A	231	406	8.4e-21	0.20	0.63		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1546	1d0b	A	269	418	2.8e-19	0.41	0.99		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1546	1d0b	A	70	207	8.4e-20	0.39	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1546	1d0b	A	86	256	7e-24	0.52	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1546	1dce	A	158	261	1.4e-13	0.60	1.00		RAB GERANYLGERANYLTRA	TRANSFERASE CRYSTAL STRUCTURE, RAB

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1546	1dce	A	227	330	1.3e-10	0.42	0.84		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1546	1dce	A	95	212	2.8e-11	0.34	0.27		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1546	1ds9	A	129	289	4.8e-17	0.18	0.82		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1546	1ds9	A	143	300	1.1e-15	-0.40	0.25		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1546	1ds9	A	210	334	2.4e-12	0.24	0.66		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1546	1ds9	A	249	354	3.6e-16	-0.71	0.33		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1546	1ds9	A	267	383	1.3e-12	-0.23	0.24		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1546	1fo1	A	194	261	1.3e-08	-0.07	0.40		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1546	1fo1	B	194	261	1.3e-08	-0.17	0.13		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1546	1fs2	A	134	325	1.4e-11	0.22	0.36		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1546	1ff8	A	194	261	1.3e-08	0.11	0.23		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RIBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
1546	1yrg	A	117	330	2.4e-21	-0.04	0.00		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1546	2bnh		136	363	1.2e-25	0.20	0.96		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1546	2bnh		68	362	6e-25	0.11	0.94		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1550	1b8q	A	69	142	5.6e-12	0.18	-0.09		NEURONAL NITRIC OXIDE SYNTHASE; CHAIN: A; HEPTAPEPTIDE; CHAIN: B;	OXIDOREDUCTASE PDZ DOMAIN, NNOS, NITRIC OXIDE SYNTHASE
1550	1be9	A	69	142	1.3e-20	0.24	-0.08		PSD-95; CHAIN: A; CRIPT; CHAIN: B;	PEPTIDE RECOGNITION PEPTIDE RECOGNITION, PROTEIN LOCALIZATION
1550	1kwa	A	73	142	9.8e-13	0.00	-0.19		HCASK/LIN-2 PROTEIN; CHAIN: A, B;	KINASE HCASK, GLGF REPEAT, DHR; PDZ DOMAIN, NEUREXIN, SYNDECAN, RECEPTOR CLUSTERING, KINASE
1550	1pdr		71	142	8.4e-20	0.18	-0.09		HUMAN DISCS LARGE PROTEIN; CHAIN: NULL;	SIGNAL TRANSDUCTION HDLG, DHR3 DOMAIN; SIGNAL TRANSDUCTION, SH3 DOMAIN, REPEAT
1550	1qav	A	69	142	2.8e-20	0.13	-0.02		ALPHA-1 SYNTROPHIN (RESIDUES 77-171); CHAIN: A; NEURONAL	MEMBRANE PROTEIN/OXIDOREDUCTASE BETA-FINGER, HETERODIMER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									NITRIC OXIDE SYNTHASE (RESIDUES 1-130); CHAIN: B;	
1550	1qlc	A	72	142	7e-18	0.01	-0.09		POSTSYNAPTIC DENSITY PROTEIN 95; CHAIN: A;	PEPTIDE RECOGNITION PSD-95; PDZ DOMAIN, NEURONAL NITRIC OXIDE SYNTHASE, NMDA RECEPTOR 2 BINDING
1551	1auo	A	358	597	2.4e-30	-0.24	0.06		CARBOXYLESTERASE; CHAIN: A, B;	HYDROLASE HYDROLASE
1551	1c1g	A	74	357	2.8e-41			97.87	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1551	1cle	A	294	595	2.8e-55	-0.17	0.00		CHOLESTEROL ESTERASE; 1CLE 4 CHAIN: A, B; 1CLE 5	LIPASE ESTERASE, SUBSTRATE/PRODUCT-BOUND 1CLE 9
1551	1din		340	597	2.4e-23	-0.25	0.25		DIENELACTONE HYDROLASE; CHAIN: NULL;	HYDROLYTIC ENZYME DLH; DIENELACTONE HYDROLASE, AROMATIC HYDROCARBON CATABOLISM, 2 SERINE ESTERASE, CARBOXYMETHYLENEBUTENOLI DASE, 3 HYDROLYTIC ENZYME
1551	1dqz	A	355	597	3.6e-30	0.05	0.30		ANTIGEN 85-C; CHAIN: A, B;	IMMUNE SYSTEM 85C ANTIGEN, 85C, MYCOBACTERIUM TUBERCULOSIS, FIBRONECTIN
1551	1ea5	A	336	597	2.4e-34	-0.06	0.11		ACETYLCHOLINESTERASE; CHAIN: A;	CHOLINESTERASE SERINE HYDROLASE, NEUROTRANSMITTER CLEAVAGE, CATALYTIC 2 TRIAD, ALPHA/BETA HYDROLASE
1551	1evq	A	352	597	2.8e-35	0.00	0.75		SERINE HYDROLASE; CHAIN: A;	HYDROLASE ALPHA/BETA HYDROLASE FOLD
1551	1f0n	A	334	597	1.2e-32	0.04	0.64		ANTIGEN 85B; CHAIN: A;	TRANSFERASE MYCOLYL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										TRANSFERASE; 30KDA SECRETORY PROTEIN; ANTIGEN 85B
1551	1f6w	A	274	580	4.2e-64	-0.02	0.16		BILE SALT ACTIVATED LIPASE; CHAIN: A;	HYDROLASE BILE SALT ACTIVATED LIPASE, ESTERASE, CATALYTIC DOMAIN
1551	1fj2	A	349	597	4.8e-32	-0.09	0.19		ACYL PROTEIN THIOESTERASE 1; CHAIN: A, B;	HYDROLASE ALPHA/BETA HYDROLASE, SERINE HYDROLASE, SAD, ANOMALOUS 2 DIFFRACTION
1551	1jkm	A	301	575	2.8e-26	-0.02	0.80		BREFELDIN A ESTERASE; CHAIN: A, B;	SERINE HYDROLASE SERINE HYDROLASE, DEGRADATION OF BREFELDIN A, ALPHA/BETA 2 HYDROLASE FAMILY
1551	1lpp		294	595	1.4e-54	-0.30	0.00		HYDROLASE LIPASE (E.C.3.1.1.3) (TRIACYLGLYCEROL LIPASE) COMPLEXED WITH 1LPP 3 HEXADECANESULFONATE 1LPP 4 1LPP 71	
1551	1maa	A	336	592	2.4e-34	-0.06	0.25		ACETYLCHOLINESTERASE; CHAIN: A, B, C, D;	HYDROLASE MACHE; HYDROLASE, SERINE ESTERASE, ACETYLCHOLINESTERASE, TETRAMER, 2 HYDROLASE FOLD, GLYCOSYLATED PROTEIN
1551	1qfm	A	1	597	5.6e-81			90.26	PROLYL OLIGOPEPTIDASE; CHAIN: A;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA- 2 PROPELLER
1551	1qfm	A	3	597	5.6e-81	-0.04	0.89		PROLYL OLIGOPEPTIDASE;	HYDROLASE PROLYL ENDOPEPTIDASE, POST-PROLINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A;	CLEAVING PROLYL OLIGOPEPTIDASE, AMNESIA, ALPHA/BETA-HYDROLASE, BETA- 2 PROPELLER
1551	1thg		284	594	2.8e-59	0.00	0.59		HYDROLASE(CARBOXYLIC ESTERASE) LIPASE (E.C.3.1.1.3) TRIACYLGLYCEROL HYDROLASE 1THG 3	
1552	1d7k	A	18	220	1.4e-59	0.22	0.77		HUMAN ORNITHINE DECARBOXYLASE; CHAIN: A, B;	LYASE ALPHA-BETA BARREL, PYRIDOXAL 5'-PHOSPHATE, SHEET-DOMAIN, 2 DECARBOXYLATION, ORNITHINE
1552	1f3t	A	18	203	1.4e-51	-0.09	0.96		ORNITHINE DECARBOXYLASE; CHAIN: A, B, C, D;	LYASE ODC; BETA-ALPHA-BARREL, MODIFIED GREEK KEY
1552	2tod	A	18	203	2.8e-51	-0.10	0.96		ORNITHINE DECARBOXYLASE; CHAIN: A, B, C, D;	BETA-SHEET LYASE POLYAMINE METABOLISM, PYRIDOXAL 5'-PHOSPHATE, ALPHA-BETA 2 BARREL, LYASE
1552	7odc	A	18	210	2.8e-60	0.08	0.81		ORNITHINE DECARBOXYLASE; CHAIN: A;	LYASE ODC, MODC, MODC'; PYRIDOXAL-5'-PHOSPHATE, PLP, GROUP IV DECARBOXYLASE, 2 POLYAMINES, PARASITICAL, CHEMOTHERAPY TARGET, ORNITHINE, 3 PUTRESCINE, A/B-BARREL, OBLIGATE, LYASE
1556	1ad0	A	382	437	0.00012	-0.61	0.30		FAB FRAGMENT, ANTIBODY A5B7; CHAIN: A, B, C, D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT
1556	1b4j	L	382	437	0.00012	-0.54	0.10		ANTIBODY; CHAIN: L, H;	ANTIBODY ENGINEERING ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODIES, 2 FAB, X-RAY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										STRUCTURES, GAMMA-INTERFERON
1556	1dee	A	382	437	0.00012	-0.42	0.55		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
1556	1igt	A	382	437	8.4e-05	-0.61	0.22		IG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1556	3fct	A	382	437	9.6e-05	-0.63	0.41		METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: A, C; METAL CHELATASE CATALYTIC ANTIBODY; CHAIN: B, D;	IMMUNE SYSTEM METAL CHELATASE, CATALYTIC ANTIBODY, FAB FRAGMENT, IMMUNE 2 SYSTEM
1557	1rth	A	206	320	0.0024	-0.42	0.39		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1557	1rth	B	206	320	0.0012	-0.32	0.51		HIV-1 REVERSE TRANSCRIPTASE; 1RTH 4 CHAIN: A, B; 1RTH 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1RTH 6 HIV-1 REVERSE TRANSCRIPTASE 1RTH 15
1557	1vrt	A	206	320	0.0024	-0.35	0.53		HIV-1 REVERSE TRANSCRIPTASE; *1VRT 4* CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE *HIV-1 RT; 1VRT 6 HIV-1 REVERSE* TRANSCRIPTASE 1VRT 15
1557	1vrt	B	206	320	0.0012	-0.54	0.36		HIV-1 REVERSE TRANSCRIPTASE; 1VRT *4* CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1559	1byg	A	149	397	1.4e-30	0.02	0.24		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1559	1cki	A	149	438	2.4e-20	0.10	0.05		CASEIN KINASE I	PHOSPHOTRANSFERASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1559	1f3m	C	130	464	1.4e-81	-0.14	0.12		DELTA; ICKI 6 CHAIN: A, B; 1CKI 7 SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	PROTEIN KINASE ICKI 18 TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1559	1fgk	A	137	384	2.8e-32	0.26	-0.01		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1559	1fgk	B	137	384	7e-36	0.09	0.74		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1559	1fmk		146	367	1.4e-32	0.22	0.04		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1559	1fmk		375	459	1.1e-08	-0.16	0.03		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1559	1how	A	148	231	2.4e-11	0.32	-0.01		SERINE/THREONINE-	TRANSFERASE KINASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN KINASE YMR216C; CHAIN: A;	
1559	1i44	A	149	231	1.2e-09	-0.26	0.47		INSULIN RECEPTOR; CHAIN: A;	TRANSFERASE IR; PROTEIN TYROSINE KINASE, PHOSPHOTRANSFERASE
1559	1ia8	A	149	462	8.4e-54	0.04	0.29		CHK1 CHECKPOINT KINASE; CHAIN: A;	TRANSFERASE PROTEIN KINASE
1559	1iep	A	156	367	5.6e-33	0.01	0.24		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1559	1kob	A	149	464	1.4e-53	-0.02	0.40		TWITCHIN; CHAIN: A, B;	KINASE KINASE, TWITCHIN, INTRASTERIC REGULATION
1559	1p38		142	231	1.2e-12	0.14	0.36		MAP KINASE P38; CHAIN: NULL;	TRANSFERASE MITOGEN ACTIVATED PROTEIN KINASE; TRANSFERASE, MAP KINASE, SERINE/THREONINE-PROTEIN KINASE, 2 P38
1559	1qcf	A	146	433	2.8e-34	0.08	-0.06		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1559	1qpc	A	147	374	2.8e-32	0.22	0.43		LCK KINASE; CHAIN: A;	TRANSFERASE ALPHA BETA FOLD
1559	1vr2	A	140	367	9.8e-34	0.05	0.15		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
1559	1vr2	A	365	460	2.8e-07	-0.22	0.13		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
1560	1atl	A	9	214	1.4e-70			94.37	ATROLYSIN C; 1ATL 4 CHAIN: A, B, C, D; 1ATL	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									5	
1560	1bkc	A	5	213	1.4e-24			52.22	TUMOR NECROSIS FACTOR-ALPHA-CONVERTING ENZYME; CHAIN: A, C, E, I;	D; 1ATL 6 ZN-ENDOPEPTIDASE TACE; ZN-ENDOPEPTIDASE, HYDROLASE, TNF-ALPHA
1560	1bud	A	9	212	4.2e-67			77.02	ACUTOLYSIN A; CHAIN: A;	TOXIN HEMORRHAGIN I, IAAH-I; METALLOPROTEINASE, SNAKE VENOM, MMP, TOXIN
1560	1cii		506	1002	2.4e-12	-0.41	0.13		COLICIN IA; CHAIN: NULL;	TRANSMEMBRANE PROTEIN COLICIN, BACTERIOCIN, ION CHANNEL FORMATION, TRANSMEMBRANE 2 PROTEIN
1560	1cun	A	636	896	0.00072	-0.03	0.05		ALPHA SPECTRIN; CHAIN: A, B, C;	STRUCTURAL PROTEIN TWO REPEATS OF SPECTRIN, ALPHA HELICAL LINKER REGION, 2 2 TANDEM 3-HELIX COILED- COILS, STRUCTURAL PROTEIN
1560	1dd5	A	36	215	0.007			51.70	RIBOSOME RECYCLING FACTOR; CHAIN: A;	RIBOSOME THREE-HELIX BUNDLE, BETA-ALPHA-BETA SANDWICH, RIBOSOME
1560	1hci	A	514	1000	1.2e-12	-0.42	0.18		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
1560	1hci	A	514	983	1.2e-12			140.65	ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1560	1hci	A	638	1060	2.4e-07	-0.12	0.68		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
1560	1htp		6	133	1.1e-52			114.21	OXIDOREDUCTASES(ACTING ON CH-NH2 DONOR) H-PROTEIN (E.C.1.4.4.2) COMPLEXED WITH LIPOIC ACID CHARGED 1HTP 3 IN METHYLAMINE 1HTP 4 1HTP 77	
1560	1hzp	A	3	356	8.4e-56			72.15	3-OXOACYL-[ACYL-CARRIER-PROTEIN] SYNTHASE III; CHAIN: A, B;	TRANSFERASE MT-FABH; FATTY ACID BIOSYNTHESIS, MYOBACTERIUM TUBERCULOSIS, 2 STRUCTURAL BASIS FOR SUBSTRATE SPECIFICITY
1560	1i84		S114	1008	1.2e-13			158.73	SMOOTH MUSCLE MYOSIN HEAVY CHAIN; CHAIN: S, V; SMOOTH MUSCLE MYOSIN ESSENTIAL LIGHT CHAIN; CHAIN: T, W; SMOOTH MUSCLE MYOSIN REGULATORY LIGHT CHAIN; CHAIN: U, Z;	CONTRACTILE PROTEIN MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE; ELC, MYOSIN ALKALI LIGHT CHAIN; RLC, MYOSIN REGULATORY LIGHT CHAIN 2, SMOOTH MUSCLE PROTEIN, SMOOTH MUSCLE, MYOSIN SUBFRAGMENT 2, HEAVY 2 MEROMYOSIN, ESSENTIAL LIGHT CHAIN, REGULATORY LIGHT CHAIN, 3 MOTOR PROTEIN, COILED-COIL
1560	1iag		5	214	1.4e-67			82.71	METALLOPROTEASE ADAMALYSIN II	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									(PROTEINASE II) (E.C.3.4.24.46) 1IAG 3	
1560	1qua	A	5	212	4.2e-65			84.37	ACUTOLYSIN-C; CHAIN: A;	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRODON ACUTUS
1560	1quu	A	525	796	0.0024	-0.27	0.05		HUMAN SKELETAL MUSCLE ALPHA-ACTININ 2; CHAIN: A;	CONTRACTILE PROTEIN TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN
1560	1ses	A	872	944	4.2e-05	0.06	-0.03		LIGASE(SYNTHETASE) SERYL-TRNA SYNTHETASE (E.C.6.1.1.11) (SERINE-TRNA LIGASE) 1SES 3 COMPLEXED WITH SERYL-HYDROXAMATE-AMP 1SES 4	
1560	1sig		514	778	6e-06	-0.29	0.05		RNA POLYMERASE PRIMARY SIGMA FACTOR; CHAIN: NULL;	TRANSCRIPTION REGULATION SIGMA70; RNA POLYMERASE SIGMA FACTOR, TRANSCRIPTION REGULATION
1568	1htp		60	187	4.8e-35			113.26	OXIDOREDUCTASES(ACTING ON CH-NH2 DONOR) H-PROTEIN (E.C.1.4.4.2) COMPLEXED WITH LIPOIC ACID CHARGED 1HTP 3 IN METHYLAMINE 1HTP 4 1HTP 77	
1568	1htp		65	183	4.8e-35	1.41	1.00		OXIDOREDUCTASES(ACTING ON CH-NH2 DONOR) H-PROTEIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									(E.C.1.4.4.2) COMPLEXED WITH LIPOIC ACID	
									CHARGED 1HTP 3 IN METHYLAMINE 1HTP 4	
1568	1htp		65	185	7e-27	1.38	1.00		1HTP 77 OXIDOREDUCTASES(ACTING ON CH-NH2	
									DONOR) H-PROTEIN (E.C.1.4.4.2) COMPLEXED	
									WITH LIPOIC ACID CHARGED 1HTP 3 IN	
									METHYLAMINE 1HTP 4 1HTP 77	
1570	1a88	A	176	385	0.0096	-0.10	0.29		CHLOROPEROXIDASE L; CHAIN: A, B, C;	HALOPEROXIDASE
										BROMOPEROXIDASE L,
										HALOPEROXIDASE L;
										HALOPEROXIDASE,
										OXIDOREDUCTASE
1570	1a8s		177	385	0.006	0.10	0.25		CHLOROPEROXIDASE F; CHAIN: NULL;	HALOPEROXIDASE
										HALOPEROXIDASE F;
										HALOPEROXIDASE,
										OXIDOREDUCTASE, PROPIONATE
										COMPLEX
1570	1din		188	431	0.006	0.11	0.10		DIENELACTONE HYDROLASE; CHAIN: NULL;	HYDROLYTIC ENZYME DLH;
										DIENELACTONE HYDROLASE,
										AROMATIC HYDROCARBON
										CATABOLISM, 2 SERINE
										ESTERASE,
										CARBOXYMETHYLENEBUTENOLIDASE, 3 HYDROLYTIC ENZYME
1572	2gli	A	586	647	1.4e-13	0.30	0.23		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1572	2gli	A	626	652	4.2e-10	0.29	0.90		ZINC FINGER PROTEIN	COMPLEX (DNA-BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									GLI1; CHAIN: A; DNA; CHAIN: C, D;	PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1575	1qfh	A	536	641	0.00096	-0.28	0.15		GELATION FACTOR; CHAIN: A, B;	ACTIN BINDING PROTEIN ACTIN BINDING PROTEIN 120; ACTIN BINDING PROTEIN, IMMUNOGLOBULIN, GELATION FACTOR, ABP- 2 120
1577	1hs6	A	34	614	4.8e-77			110.77	LEUKOTRIENE A-4 HYDROLASE; CHAIN: A;	HYDROLASE PROTEIN-INHIBITOR COMPLEX, ALPHA-BETA PROTEIN
1577	1hs6	A	41	594	4.8e-77	0.24	0.47		LEUKOTRIENE A-4 HYDROLASE; CHAIN: A;	HYDROLASE PROTEIN-INHIBITOR COMPLEX, ALPHA-BETA PROTEIN
1577	1hs6	A	47	505	1.3e-78	0.22	0.69		LEUKOTRIENE A-4 HYDROLASE; CHAIN: A;	HYDROLASE PROTEIN-INHIBITOR COMPLEX, ALPHA-BETA PROTEIN
1579	1b7f	A	821	939	1.3e-15	0.26	0.95		SXL-LETHAL PROTEIN; CHAIN: A, B; RNA (5'-R(P*GP*UP*UP*GP*UP*UP*UP*UP*UP*UP*U)- CHAIN: P, Q;	RNA-BINDING PROTEIN/RNA TRA PRE-MRNA; SPLICING REGULATION, RNP DOMAIN, RNA COMPLEX
1579	1cvj	A	823	934	1.4e-15	0.47	0.65		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1579	1cvj	B	721	878	1.4e-30	0.01	-0.17		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									R(*AP*AP*AP*AP*AP*A P*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	
1579	1cvj	F	823	938	9.8e-16	0.30	0.39		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*A P*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1579	1cvj	H	823	938	9.8e-16	0.26	0.72		POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*A P*AP*AP*AP*AP*A)-3'); CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1579	1fxl	A	821	940	5.6e-19	0.17	0.99		PARANEOPLASTIC ENCEPHALOMYELITIS ANTIGEN HUD; CHAIN: A; 5'-R(P*UP*UP*UP*UP*AP* UP*UP*UP*U)-3'; CHAIN: B;	TRANSCRIPTION/RNA HUD, HU-ANTIGEN D; PROTEIN-RNA COMPLEX, HUD, AU-RICH ELEMENT
1579	1ha1		721	894	2.8e-42	0.09	-0.12		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1579	1ha1		821	939	2.8e-25	0.14	0.89		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1579	1hd0	A	822	894	8.4e-17	0.31	1.00		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN D0; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1579	2mss	A	822	894	2.8e-15	0.34	0.94		MUSASHI1; CHAIN: A;	RNA BINDING PROTEIN RNA-BINDING DOMAIN
1579	2up1	A	721	894	2.8e-44	0.09	-0.11		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1579	2up1	A	821	939	1.1e-24	0.27	0.89		HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1579	3sxl	A	821	939	9.8e-16	0.16	0.93		SEX-LETHAL; CHAIN: A, B, C;	RNA BINDING DOMAIN RNA BINDING DOMAIN, RBD, RNA RECOGNITION MOTIF, RRM, 2 SPLICING INHIBITOR, TRANSLATIONAL INHIBITOR, SEX 3 DETERMINATION, X CHROMOSOME DOSAGE COMPENSATION
1580	1a7c	A	267	544	2.8e-62	-0.24	0.12		PLASMINOGEN	COMPLEX (PROTEASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	INHIBITOR/PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
1580	1a7c	A	34	337	7e-72	0.04	1.00		PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
1580	1a7c	A	8	225	1.4e-62			59.79	PLASMINOGEN ACTIVATOR INHIBITOR TYPE 1; CHAIN: A; PENTAPEPTIDE; CHAIN: B, C	COMPLEX (PROTEASE INHIBITOR/PEPTIDE) PAI-1; SERINE PROTEASE INHIBITOR, PAI-1, CARBOHYDRATE, INHIBITOR 2 COMPLEX, PEPTIDE
1580	1as4	A	39	374	1.1e-80			94.64	ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
1580	1as4	A	40	309	1.1e-80	0.04	1.00		ANTICHYMOTRYPSIN; CHAIN: A, B;	SERPIN ACT; SERPIN, SERINE PROTEASE INHIBITOR, ANTICHYMOTRYPSIN
1580	1ath	A	31	405	2.8e-66			132.53	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1580	1ath	B	30	388	4.2e-67			119.29	HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1580	1ath	B	38	309	4.2e-67	0.07	1.00		HUMAN ANTITHROMBIN-III ANTITHROMBIN III 1ATH 3	
1580	1by7	A	38	402	7e-66			104.95	PLASMINOGEN ACTIVATOR INHIBITOR-	PROTEIN BINDING PAI-2; SERPIN, PROTEIN BINDING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1580	1db2	A	267	544	1.4e-68	0.01	0.59		2; CHAIN: A; PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1580	1db2	A	35	335	4.2e-71	0.02	0.96		PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1580	1db2	A	9	225	2.8e-61			50.63	PLASMINOGEN ACTIVATOR INHIBITOR-1; CHAIN: A, B;	HYDROLASE INHIBITOR NATIVE SERPIN, HYDROLASE INHIBITOR
1580	1dzg	I	1	405	1.4e-67			136.83	ANTITHROMBIN-III; CHAIN: I; ANTITHROMBIN-III; CHAIN: L;	SERPIN SERPIN
1580	1dzg	I	6	306	1.4e-67	-0.03	0.92		ANTITHROMBIN-III; CHAIN: I; ANTITHROMBIN-III; CHAIN: L;	SERPIN SERPIN
1580	1ezx	A	39	307	2.8e-80	-0.06	0.90		ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
1580	1ezx	A	39	375	2.8e-80			110.88	ALPHA-1-ANTITRYPSIN; CHAIN: A; ALPHA-1-ANTITRYPSIN; CHAIN: B; TRYPSIN; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR PROTEASE-INHIBITOR COMPLEX, SERPIN, ALPHA-1-ANTITRYPSIN, 2 TRYPSIN
1580	1hle	A	37	309	1.4e-77	0.25	0.94		HYDROLASE INHIBITOR(SERINE PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
1580	1hle	A	38	378	1.4e-77			111.65	HYDROLASE INHIBITOR(SERINE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEINASE) HORSE LEUKOCYTE ELASTASE INHIBITOR (HLE) 1HLE 3	
1580	1i99	I	267	544	9.8e-61	-0.26	0.24		ALASERPIN; CHAIN: I; TRYPSIN II, ANIONIC; CHAIN: E;	HYDROLASE/HYDROLASE INHIBITOR SERPIN 1; PRETRYPSINOGEN II; MICHAELIS SERPIN-PROTEASE COMPLEX INHIBITORY TRIAD
1580	1i99	I	352	537	7.2e-31	-0.12	0.18		ALASERPIN; CHAIN: I; TRYPSIN II, ANIONIC; CHAIN: E;	HYDROLASE/HYDROLASE INHIBITOR SERPIN 1; PRETRYPSINOGEN II; MICHAELIS SERPIN-PROTEASE COMPLEX INHIBITORY TRIAD
1580	1ova	A	234	544	5.6e-70	-0.24	0.51		SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
1580	1ova	A	39	304	5.6e-67	0.03	1.00		SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
1580	1ova	A	39	402	5.6e-67			108.90	SERPIN OVALBUMIN (EGG ALBUMIN) 1OVA 3	
1580	1qlp	A	35	390	2.8e-80			107.96	ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN, GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1580	1qlp	A	39	307	2.8e-80	-0.02	0.89		ALPHA-1-ANTITRYPSIN; CHAIN: A;	SERINE PROTEASE INHIBITOR ALPHA-1-PROTEINASE INHIBITOR, ALPHA-1-ANTIPROTEINASE; SERINE PROTEASE INHIBITOR, SERPIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										GLYCOPROTEIN, SIGNAL, 2 POLYMORPHISM, EMPHYSEMA, DISEASE MUTATION, ACUTE PHASE
1580	1qmn	A	181	544	9.8e-65	-0.06	0.11		ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1580	1qmn	A	40	309	1.1e-78	0.04	0.99		ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1580	1qmn	A	40	404	1.1e-78			118.53	ALPHA-1-ANTICHYMOTRYPSIN; CHAIN: A;	SERPIN AACT SERPIN, SERINE PROTEINASE INHIBITOR, PARTIAL LOOP 2 INSERTION, LOOP-SHEET POLYMERIZATION, EMPHYSEMA, DISEASE 3 MUTATION, ACUTE PHASE PROTEIN, CONFORMATIONAL DISEASE
1580	1sek		267	544	1.1e-59	-0.29	0.24		SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
1580	1sek		33	388	2.8e-63			140.59	SERPIN K; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, SERPIN, PROTEASE
1582	1a4y	A	188	493	1.4e-12	-0.03	0.60		RIBONUCLEASE	COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	(INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1582	1a4y	A	54	371	2.4e-36	-0.13	0.18		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1582	1a9n	A	171	320	1.2e-21	0.51	0.42		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	A	192	298	4.2e-07	0.71	0.47		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	A	220	372	1.2e-18	0.25	0.07		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	A	247	378	8.4e-20	0.29	0.30		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	A	288	396	0.00014	-0.17	0.11		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1582	1a9n	A	51	134	2.4e-07	0.06	0.41		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	A	51	154	5.6e-07	0.11	0.31		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	A	76	218	4.8e-26	0.46	0.54		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	171	320	2.4e-22	0.37	0.39		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	192	298	4.2e-07	0.58	0.36		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	220	372	2.4e-18	0.26	0.05		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	247	378	4.8e-20	0.16	0.22		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	288	396	0.00014	0.15	0.46		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	51	154	5.6e-07	0.20	0.34		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A';	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, C; U2 B"; CHAIN: B, D;	(NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1a9n	C	76	250	9.6e-28	0.38	0.34		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1582	1cs6	A	429	601	2.8e-14	0.30	0.29		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1582	1cvs	C	440	603	4.2e-11	0.06	-0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1582	1cvs	D	430	514	4.8e-15	-0.06	0.75		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1582	1d0b	A	116	320	8.4e-27	0.52	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1582	1d0b	A	162	369	9.6e-23	0.17	0.83		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1582	1d0b	A	236	416	2.8e-19	0.17	0.99		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1582	1d0b	A	79	268	2.8e-26	0.34	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1582	1dce	A	185	273	2.8e-12	0.57	1.00		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1582	1dce	A	216	340	2.8e-13	0.37	0.96		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1582	1dce	A	288	395	1.4e-08	0.16	0.95		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1582	1dce	A	42	129	4.2e-09	-0.28	0.84		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1582	1dce	A	51	268	3.6e-25	-0.32	0.00		RAB GERANYLGERANYLTRA NSFERASE ALPHA	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1582	1ds9	A	199	362	8.4e-15	-0.13	0.48		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1582	1ds9	A	225	365	1.4e-12	-0.43	0.19		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1582	1ds9	A	239	371	2.4e-14	-0.32	0.10		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1582	1ds9	A	45	153	8.4e-11	-0.21	0.04		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1582	1ds9	A	92	274	7.2e-23	-0.16	0.15		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1582	1epf	A	432	514	3.6e-15	0.28	0.89		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1582	1ev2	E	439	586	5.6e-12	0.15	-0.05		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1582	1ev2	G	439	586	7e-12	0.08	-0.08		FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1582	1evt	C	440	586	1.4e-11	0.09	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1582	1fhg	A	415	514	2.4e-18	-0.15	0.46		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1582	1fna		531	593	0.006	0.22	0.06		CELL ADHESION PROTEIN FIBRONECTIN CELL-ADHESION MODULE TYPE III-10 1FNA 3	
1582	1fnf		454	595	2.8e-05	0.21	-0.01		FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1582	1fo1	A	308	371	0.00012	-0.53	0.17		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1582	1fo1	A	50	147	1.4e-07	-0.19	0.24		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										(RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1582	1fo1	B	333	425	1.1e-07	-0.01	0.17		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1582	1fo1	B	50	147	1.4e-07	-0.06	0.24		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1582	1fo1	B	91	194	2.4e-13	-0.68	0.12		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1582	1fqv	A	192	368	1.4e-15	0.48	0.75		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1582	1fs2	A	110	362	4.8e-16	-0.05	0.09		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1582	1fs2	A	192	368	1.4e-15	0.40	0.89		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1582	1fs2	A	72	288	1.2e-12	-0.11	0.06		SKP2; CHAIN: A, C; SKP1;	LIGASE CYCLIN A/CDK2-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B, D;	ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1582	1ft8	A	333	425	1.1e-07	-0.06	0.11		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RIBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
1582	1ft8	A	50	147	1.4e-07	-0.06	0.09		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RIBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
1582	1ie5	A	422	514	6e-19	0.07	0.24		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE IMMUNOGLOBULIN FOLD
1582	1iil	G	422	514	1.2e-15	0.11	0.98		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1582	1iil	G	439	586	5.6e-11	-0.05	0.00		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1582	1mfn		504	597	0.0059	0.22	-0.06		FIBRONECTIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN, RGD, EXTRACELLULAR MATRIX, 2 HEPARIN-BINDING, GLYCOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1582	1nct		422	514	1.2e-17	0.06	0.19		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1582	1ten		531	593	0.0096	0.12	0.05		CELL ADHESION PROTEIN TENASCIN (THIRD FIBRONECTIN TYPE III REPEAT) 1TEN 3	
1582	1tnm		430	514	1.1e-17	0.08	0.37		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1582	1vca	A	430	585	4.8e-11	0.11	0.18		HUMAN VASCULAR CELL ADHESION MOLECULE-1; 1VCA 4 CHAIN: A, B; 1VCA 5	CELL ADHESION PROTEIN VCAM-D1,2; 1VCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING 1VCA 15
1582	1wit		430	514	1.2e-15	0.27	-0.07		TWITCHIN 18TH IGSF MODULE; CHAIN: NULL;	MUSCLE PROTEIN IMMUNOGLOBULIN SUPERFAMILY, I SET, MUSCLE PROTEIN
1582	1yrg	A	180	372	4.2e-11	0.27	0.87		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SP11, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1582	1yrg	A	40	202	1.4e-06	-0.32	0.23		GTPASE-ACTIVATING	TRANSCRIPTION RNA1P;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN RNA1_SCHPO; CHAIN: A, B;	RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1582	1yrg	A	72	202	6e-14	0.01	0.05		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1582	1yrg	A	87	320	2.4e-30	0.39	0.86		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1582	2bnh		188	472	4.2e-15	0.11	0.62		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1582	2bnh		40	457	1.4e-20	-0.06	0.21		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										LEUCINE-RICH REPEATS
1582	2bnh		55	375	2.4e-37	0.07	0.39		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1582	2ncm		430	514	4.8e-17	0.26	0.98		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1582	3ncm	A	430	514	8.4e-18	0.45	0.83		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1585	1lxa		364	470	3.6e-05	1.02	0.36		UDP N-ACETYLGLUCOSAMINE O-ACYLTRANSFERASE; 1LXA 5 CHAIN: NULL; 1LXA 6	ACYLTRANSFERASE LPXA; 1LXA 7 TRANSFERASE, ACYLTRANSFERASE, LIPID A BIOSYNTHESIS, 1LXA 17 2 LIPID SYNTHESIS 1LXA 18
1585	1qre	A	364	470	0.00012	0.73	0.65		CARBONIC ANHYDRASE; CHAIN: A;	LYASE BETA-HELIX
1585	1xat		364	475	0.0072	0.70	-0.09		XENOBIOTIC ACETYLTRANSFERASE; CHAIN: NULL;	ACETYLTRANSFERASE ACETYLTRANSFERASE, XENOBIOTIC, CHLORAMPHENICOL, LEFT-HANDED 2 BETA HELIX
1587	1bor		171	208	0.00028	-0.25	0.09		TRANSCRIPTION	TRANSCRIPTION REGULATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FACTOR PML; CHAIN: NULL;	PROTO-ONCOGENE, NUCLEAR BODIES (PODS), LEUKEMIA, 2 TRANSCRIPTION REGULATION
1591	1a17		252	393	2.8e-30	0.09	1.00		SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE
1591	1b3u	A	142	751	2.4e-13			112.25	PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1591	1b3u	A	193	804	2.4e-13	0.03	0.88		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1591	1c1g	A	1	249	8.4e-05			50.04	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1591	1ee4	A	396	800	3.6e-16	0.47	1.00		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1591	1ee4	A	635	816	1.2e-08	0.11	0.83		KARYOPHERIN ALPHA; CHAIN: A, B; MYC PROTO-ONCOGENE PROTEIN; CHAIN: C, D, E, F;	TRANSPORT PROTEIN SERINE-RICH RNA POLYMERASE I SUPPRESSOR PROTEIN; ARM REPEAT
1591	1elr	A	252	371	2.8e-20	0.13	0.99		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1591	1elr	A	256	371	1.2e-24	0.38	0.98		CHAIN: B; TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1591	1elw	A	231	322	4.2e-13	-0.34	0.13		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1591	1elw	A	252	368	8.4e-24	0.33	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1591	1elw	A	252	371	1.1e-26	0.32	1.00		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1591	1elw	A	299	399	1.4e-11	-0.51	0.23		TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1591	1fch	A	231	477	1.4e-31	-0.30	0.05		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1591	1g3j	C	461	802	2.4e-14	0.13	0.46		BETA-CATENIN ARMADILLO REPEAT REGION; CHAIN: A, C; TCF3-CBD (CATENIN BINDING DOMAIN); CHAIN: B, D;	TRANSCRIPTION BETA-CATENIN,TCF-3, PROTEIN-PROTEIN COMPLEX
1591	1g3j	C	476	796	8.4e-11	0.34	0.64		BETA-CATENIN	TRANSCRIPTION BETA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ARMADILLO REPEAT REGION; CHAIN: A, C; TCF3-CBD (CATENIN BINDING DOMAIN); CHAIN: B, D;	CATENIN,TCF-3, PROTEIN-PROTEIN COMPLEX
1591	1hh8	A	253	443	2.8e-15	-0.30	0.19		NEUTROPHIL CYTOSOL FACTOR 2; CHAIN: A;	PHAGOCYTE OXIDASE FACTOR P67PHOX, NCF-2; PHAGOCYTE OXIDASE FACTOR, SH3 DOMAIN, REPEAT, TPR REPEAT
1591	1i7w	A	382	757	4.8e-07	0.10	0.77		BETA-CATENIN; CHAIN: A, C; EPITHELIAL-CADHERIN; CHAIN: B, D;	CELL ADHESION E-CADHERIN; E-CADHERIN, CELL ADHESION, BETA-CATENIN, PROTEIN-PROTEIN 2 COMPLEX, EXTENDED INTERFACE, ARMADILLO REPEAT, PHOSPHOSERINE
1591	1i7w	A	591	812	4.8e-06	0.32	0.96		BETA-CATENIN; CHAIN: A, C; EPITHELIAL-CADHERIN; CHAIN: B, D;	CELL ADHESION E-CADHERIN; E-CADHERIN, CELL ADHESION, BETA-CATENIN, PROTEIN-PROTEIN 2 COMPLEX, EXTENDED INTERFACE, ARMADILLO REPEAT, PHOSPHOSERINE
1591	1i7w	A	676	806	9.6e-05	0.22	0.89		BETA-CATENIN; CHAIN: A, C; EPITHELIAL-CADHERIN; CHAIN: B, D;	CELL ADHESION E-CADHERIN; E-CADHERIN, CELL ADHESION, BETA-CATENIN, PROTEIN-PROTEIN 2 COMPLEX, EXTENDED INTERFACE, ARMADILLO REPEAT, PHOSPHOSERINE
1591	1ial	A	426	806	4.8e-16	0.19	0.43		IMPORTIN ALPHA; CHAIN: A;	NUCLEAR IMPORT RECEPTOR KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1591	1ial	A	733	812	1.2e-06	0.29	0.12		IMPORTIN ALPHA;	NUCLEAR IMPORT RECEPTOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A;	KARYOPHERIN ALPHA; NUCLEAR IMPORT RECEPTOR, NUCLEAR LOCALIZATION SIGNAL, 2 ARMADILLO REPEATS, AUTOINHIBITION, INTRASTERIC REGULATION
1591	1ibr	B	732	806	7.2e-05	-0.29	0.17		RAN; CHAIN: A, C; IMPORTIN BETA SUBUNIT; CHAIN: B, D;	SMALL GTPASE KARYOPHERIN BETA, P95 SMALL GTPASE, NUCLEAR TRANSPORT RECEPTOR
1591	1ihg	A	232	321	9.8e-11	-0.03	0.16		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRATRICOPEPTIDE
1591	1ihg	A	255	380	8.4e-24	0.00	1.00		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRATRICOPEPTIDE
1591	1ihg	A	256	353	7.2e-25	0.48	1.00		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRATRICOPEPTIDE
1591	3bct		396	801	3.6e-16	0.25	0.83		BETA-CATENIN; CHAIN: NULL;	ARMADILLO REPEAT ARMADILLO REPEAT, BETA-CATENIN, CYTOSKELETON
1592	1f62	A	1117	1161	0.0048	-0.52	0.21		TRANSCRIPTION FACTOR WSTF; CHAIN: A;	TRANSCRIPTION ZN-FINGER
1593	1aa8	A	195	518	1.2e-05	0.89	0.06		D-AMINO ACID OXIDASE; CHAIN: A, B;	OXIDASE FAD, OXIDASE, D-AMINO ACID
1593	1ak5		491	679	0.0024	0.77	-0.13		INOSINE-5'-MONOPHOSPHATE DEHYDROGENASE; CHAIN: NULL;	OXIDOREDUCTASE IMPDH; DEHYDROGENASE, ALPHA-8-BETA-8 BARREL, TIM BARREL, PURINE 2 METABOLISM,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1593	1b3o	A	363	543	0.00048	0.81	-0.05		INOSINE MONOPHOSPHATE DEHYDROGENASE 2; CHAIN: A, B;	OXIDOREDUCTASE, TETRAMER, C4-TETRAMER
1593	1b3o	B	300	545	1.2e-06	0.65	-0.14			DEHYDROGENASE IMPD, IMPDH; DEHYDROGENASE, IMPD, IMPDH, GUANINE NUCLEOTIDE SYNTHESIS
1593	1b65	A	458	670	3.6e-07	0.39	-0.06		INOSINE MONOPHOSPHATE DEHYDROGENASE 2; CHAIN: A, B; AMINOPEPTIDASE; CHAIN: A, B, C, D, E, F;	DEHYDROGENASE IMPD, IMPDH; DEHYDROGENASE, IMPD, IMPDH, GUANINE NUCLEOTIDE SYNTHESIS HYDROLASE DMPA; HYDROLASE, PEPTIDE DEGRADATION, NTN HYDROLASE
1593	1b8t	A	841	867	1.2e-07	-0.47	0.31		CRP1; CHAIN: A;	CONTRACTILE LIM DOMAIN, CRP, NMR, MUSCLE DIFFERENTIATION, CONTRACTILE
1593	1be3	D	753	852	0.0024	0.40	0.15		CYTOCHROME BC1 COMPLEX; CHAIN: A, B, C, D, E, F, G, H, I, J, K;	ELECTRON TRANSPORT UBIQUINOL CYTOCHROME C OXIDOREDUCTASE, COMPLEX ELECTRON TRANSPORT, CYTOCHROME, MEMBRANE PROTEIN
1593	1cex		141	339	8.4e-15	0.95	0.30		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		174	391	4.8e-14	1.07	-0.15		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		244	455	4.8e-18	0.98	0.45		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		293	526	6e-20	0.80	0.00		CUTINASE; CHAIN:	SERINE ESTERASE HYDROLASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									NULL;	SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		373	565	1.1e-16	0.77	-0.20		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		410	619	2.4e-16	0.48	-0.19		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		419	596	1.1e-16	0.48	-0.19		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		488	668	2.4e-13	0.19	-0.19		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		530	772	3.6e-13	0.24	-0.19		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1cex		578	836	6e-12	0.09	-0.19		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1593	1d0s	A	488	818	0.0036	0.57	0.17		NICOTINATE MONONUCLEOTIDE:5,6-DIMETHYLBENZIMIDAZOLE PHOSPHORIBOSYLTRANSFERASE	TRANSFERASE DINUCLEOTIDE-BINDING MOTIF, PHOSPHORIBOSYL
1593	1dbi	A	140	401	6e-12	1.13	-0.15		AK.1 SERINE PROTEASE; CHAIN: A	HYDROLASE HYDROLASE
1593	1dbi	A	216	485	1.1e-10	0.80	-0.12		AK.1 SERINE PROTEASE; CHAIN: A	HYDROLASE HYDROLASE
1593	1dbi	A	347	635	3.6e-12	0.84	-0.17		AK.1 SERINE PROTEASE; CHAIN: A	HYDROLASE HYDROLASE
1593	1dbi	A	411	662	6e-12	0.61	-0.18		AK.1 SERINE PROTEASE; CHAIN: A	HYDROLASE HYDROLASE
1593	1dvj	B	302	463	0.00072	0.88	0.00		OROTIDINE 5'-PHOSPHATE	LYASE OMPDECASE; TIM BARREL, DIMER

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									DECARBOXYLASE; CHAIN: A, B, C, D;	
1593	1eep	A	330	474	0.00012	0.88	0.59		INOSINE 5'-MONOPHOSPHATE DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE ALPHA-BETA BARREL, TIM BARREL, IMPDH, IMP DEHYDROGENASE, 2 LOOP-6, PURINE BIOSYNTHESIS
1593	1eua	A	196	393	1.1e-06	0.57	-0.14		KDPG ALDOLASE; CHAIN: A, B, C;	LYASE BETA BARREL, TRIMER, CARBINOLAMINE
1593	1eua	A	312	464	2.4e-06	0.77	-0.12		KDPG ALDOLASE; CHAIN: A, B, C;	LYASE BETA BARREL, TRIMER, CARBINOLAMINE
1593	1eua	A	321	539	6e-09	1.18	0.34		KDPG ALDOLASE; CHAIN: A, B, C;	LYASE BETA BARREL, TRIMER, CARBINOLAMINE
1593	1fcb	A	375	474	4.8e-05	0.87	-0.08		OXIDOREDUCTASE (CH-OH(D)-CYTOCHROME(A)) FLAVOCYTOCHROME $B=2= (E.C.1.1.2.3) 1FCB 3	
1593	1fcb	B	303	548	8.4e-18	0.95	0.11		OXIDOREDUCTASE (CH-OH(D)-CYTOCHROME(A)) FLAVOCYTOCHROME $B=2= (E.C.1.1.2.3) 1FCB 3	
1593	1ff9	A	310	515	0.00024	0.60	-0.14		SACCHAROPINE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE LYSINE BIOSYNTHESIS, ALPHA-AMINOADIPATE PATHWAY, 2 SACCHAROPINE REDUCTASE, DEHYDROGENASE
1593	1foh	A	171	798	3.6e-36	0.63	-0.17		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE, OXIDOREDUCTASE
1593	1foh	A	1	619	2.4e-30	0.49	-0.19		PHENOL	FLAVIN FLAVIN, PHENOL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HYDROXYLASE; CHAIN: A, B, C, D;	HYDROXYLASE, MONOOXYGENASE, OXIDOREDUCTASE
1593	1fob	A	351	824	7.2e-19	0.76	-0.18		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE, OXIDOREDUCTASE
1593	1ga6	A	140	524	7.2e-16	0.48	-0.18		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPEPSIN, PEPSTATIN-INSENSITIVE SERINE-CARBOXYL PROTEINASE
1593	1ga6	A	202	549	4.8e-20	0.83	0.40		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPEPSIN, PEPSTATIN-INSENSITIVE SERINE-CARBOXYL PROTEINASE
1593	1ga6	A	300	607	4.8e-19	0.75	-0.14		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPEPSIN, PEPSTATIN-INSENSITIVE SERINE-CARBOXYL PROTEINASE
1593	1ga6	A	469	819	2.4e-11	0.65	-0.18		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPEPSIN, PEPSTATIN-INSENSITIVE SERINE-CARBOXYL PROTEINASE
1593	1geq	A	303	394	0.0024	0.76	-0.09		TRYPTOPHAN SYNTHASE ALPHA-SUBUNIT; CHAIN: A, B;	LYASE TRYPTOPHAN SYNTHASE ALPHA-SUBUNIT, HYPERTHERMOPHILE, 2 PYROCOCCUS FURIOSUS, X-RAY ANALYSIS, STABILITY, CALORIMETRY
1593	1iml		839	867	8.4e-09	-0.27	0.21		CYSTEINE RICH INTESTINAL PROTEIN; CHAIN: NULL;	METAL-BINDING PROTEIN CRIP; METAL-BINDING PROTEIN, LIM DOMAIN PROTEIN
1593	1kap	P	140	481	1.1e-10	0.76	-0.20		ALKALINE PROTEASE; 1KAP 4 CHAIN: P; 1KAP 5	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									TETRAPEPTIDE (GLY SER ASN SER); 1KAP 9 CHAIN: I; 1KAP 10	PROTEASE; 1KAP 6 CALCIUM BINDING PROTEIN 1KAP 19
1593	1kap	P	286	661	2.4e-13	0.73	-0.20		ALKALINE PROTEASE; 1KAP 4 CHAIN: P; 1KAP 5 TETRAPEPTIDE (GLY SER ASN SER); 1KAP 9 CHAIN: I; 1KAP 10	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE PROTEASE; 1KAP 6 CALCIUM BINDING PROTEIN 1KAP 19
1593	1lxa		544	644	0.0096	1.66	-0.17		UDP N-ACETYLGLUCOSAMINE O-ACYLTRANSFERASE; 1LXA 5 CHAIN: NULL; 1LXA 6	ACYLTRANSFERASE LPXA; 1LXA 7 TRANSFERASE, ACYLTRANSFERASE, LIPID A BIOSYNTHESIS, 1LXA 17 2 LIPID SYNTHESIS 1LXA 18
1593	1pvd	A	324	515	0.0048	0.79	-0.12		LYASE (CARBON-CARBON) PYRUVATE DECARBOXYLASE (PDC) (E.C.4.1.1.1) 1PVD 3	
1593	1qq4	A	287	432	0.00024	0.68	-0.17		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1593	1qq4	A	338	525	8.4e-09	1.09	-0.05		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1593	1qq4	A	403	616	4.8e-05	0.98	-0.01		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1593	1qq4	A	462	660	1.2e-07	0.82	0.03		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1593	1tal		210	411	1.1e-08	0.59	-0.18		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1593	1tal		299	525	2.4e-10	1.07	-0.20		ALPHA-LYTIC	SERINE PROTEASE SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEASE; CHAIN: NULL;	PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1593	1tal		416	660	2.4e-08	0.75	-0.19		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1593	1zfj	A	358	474	0.0024	0.83	0.25		INOSINE MONOPHOSPHATE DEHYDROGENASE; CHAIN: A;	OXIDOREDUCTASE IMPDH, DEHYDROGENASE, CBS DOMAINS
1593	1zfo		841	866	0.00096	-0.18	0.39		LASP-1; CHAIN: NULL;	METAL-BINDING PROTEIN LIM DOMAIN, ZINC-FINGER, METAL-BINDING PROTEIN
1595	1bqb	A	62	350	0.0081			60.30	AUREOLYSIN; CHAIN: A;	HYDROLASE STAPHYLOCOCCUS AUREUS METALLOPROTEINASE; HYDROLASE, METALLOPROTEINASE
1595	1byn	A	18	148	4.2e-49			53.77	SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1595	1hs6	A	105	341	2.4e-73	-0.23	0.86		LEUKOTRIENE A-4 HYDROLASE; CHAIN: A;	HYDROLASE PROTEIN-INHIBITOR COMPLEX, ALPHA-BETA PROTEIN
1595	1hs6	A	15	338	1.4e-62	0.05	0.12		LEUKOTRIENE A-4 HYDROLASE; CHAIN: A;	HYDROLASE PROTEIN-INHIBITOR COMPLEX, ALPHA-BETA PROTEIN
1595	1rsy		13	146	5.6e-49			62.38	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1599	1a25	A	425	558	2.8e-31	0.16	0.82		(CALB) 1RSY 3 PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1599	1byn	A	425	556	8.4e-38	0.49	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1599	1cjy	A	440	538	1.1e-14	0.05	-0.03		CYTOSOLIC PHOSPHOLIPASE A2; CHAIN: A, B;	HYDROLASE CPLA2; PHOSPHOLIPASE, LIPID-BINDING, HYDROLASE
1599	1dqv	A	427	621	5.6e-43	0.05	0.70		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1599	1dsy	A	425	569	8.4e-32	0.48	0.99		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
1599	1rsy		421	553	4.2e-38	0.28	1.00		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1599	3rpb	A	427	561	1.4e-32	0.56	0.74		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1600	1icf	I	35	121	1.1e-17	0.08	0.28		CATHEPSIN L: HEAVY	HYDROLASE II FRAGMENT, CD74

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN; CHAIN: A, C; CATHEPSIN L: LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN;	FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
1604	1a6v	L	20	148	7e-30	0.00	-0.17		CHAIN: L, J; B1-8; CHAIN: L, H, M, I, N, J;	IMMUNOGLOBULIN
1604	1adq	L	23	121	8.4e-21	0.06	0.03		IGG4 REA; CHAIN: A; RF-AN IGM/LAMBDA; CHAIN: H, L;	IMMUNOGLOBULIN, HAPTEN COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN) COMPLEX (IMMUNOGLOBULIN/AUTOANTIGEN), RHEUMATOID FACTOR 2 AUTO-ANTIBODY COMPLEX
1604	1b2w	L	23	70	9.6e-16	0.06	0.80		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
1604	1cd0	A	21	143	1.4e-39			51.07	JTO, A VARIABLE DOMAIN FROM LAMBDA-6 TYPE CHAIN: A, B;	IMMUNE SYSTEM IMMUNOGLOBULIN, BENCE-JONES PROTEIN, LAMDA-6
1604	1cd0	A	23	72	2.4e-25	-0.52	0.41		JTO, A VARIABLE DOMAIN FROM LAMBDA-6 TYPE CHAIN: A, B;	IMMUNE SYSTEM IMMUNOGLOBULIN, BENCE-JONES PROTEIN, LAMDA-6
1604	1dl7	L	20	148	4.2e-27	0.06	-0.19		ANTIBODY M3C65 (LIGHT CHAIN); CHAIN: L; ANTIBODY M3C65 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM SINGLE CHAIN FV, REPERTOIRE SHIFT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1604	1dl7	L	20	72	2.4e-29	-0.09	0.01		ANTIBODY M3C65 (LIGHT CHAIN); CHAIN: L; ANTIBODY M3C65 (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM SINGLE CHAIN FV, REPERTOIRE SHIFT
1604	1fvd	A	23	70	1.2e-15	-0.15	0.29		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1604	1mfa		20	151	7e-30	0.03	-0.19		IMMUNOGLOBULIN FV FRAGMENT (MURINE SE155-4) COMPLEX WITH THE TRISACCHARIDE: 1MFA 3 ALPHA-D-GALACTOSE(1-2)[ALPHA-D-ABEQUOSE(1-3)]ALPHA-1MFA 4 D-MANNOSE (P1-OME) (PART OF THE CELL-SURFACE CARBOHYDRATE 1MFA 5 OF PATHOGENIC SALMONELLA) 1MFA 6	
1604	2cd0	A	23	72	2.4e-25	-0.07	0.28		BENCE-JONES PROTEIN WIL, A VARIABLE DOMAIN FROM CHAIN: A, B;	IMMUNE SYSTEM IMMUNOGLOBULIN, BENCE-JONES PROTEIN, LAMBDA-6
1604	2rhe		15	152	2.8e-45	0.00	-0.08		IMMUNOGLOBULIN BENCE-*JONES PROTEIN (LAMBDA, VARIABLE DOMAIN) 2RHE 4	
1604	2rhe		20	161	2.8e-45			67.29	IMMUNOGLOBULIN BENCE-*JONES PROTEIN (LAMBDA, VARIABLE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									DOMAIN) 2RHE 4	
1604	7fab	L	20	170	2.8e-52			57.34	IMMUNOGLOBULIN IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
1605	1chc		581	653	0.00096	-0.23	0.07		VIRUS EQUINE HERPES VIRUS-1 (C3HC4, OR RING DOMAIN) 1CHC 3 (NMR, 1 STRUCTURE) 1CHC 4	
1606	1a4y	A	571	833	7e-13	0.16	0.98		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1606	1a4y	A	623	809	1.1e-15	0.38	0.95		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1606	1a9n	A	624	779	1.2e-05	-0.21	0.34		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1606	1a9n	A	694	810	0.00072	-0.14	0.06		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1606	1brf	A	232	273	0.0084	-0.86	0.21		RUBREDOXIN; CHAIN: A;	ELECTRON TRANSPORT PF RD IRON-SULFUR PROTEIN, HIGH-RESOLUTION STRUCTURE DBREF REMARK
1606	1d0b	A	644	795	1.1e-08	-0.00	0.41		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1606	1ds9	A	701	820	7e-05	-0.12	0.65		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1606	1fo1	A	622	769	0.0029	0.10	0.11		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1606	1fqv	A	556	823	2.8e-36	0.11	0.84		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1606	1fqv	A	764	832	0.00011	0.11	0.12		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1606	1fs1	A	548	597	2.4e-10	-0.46	0.06		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1606	1fs1	A	557	597	4.2e-11	-0.32	0.77		CYCLIN A/CDK2-ASSOCIATED P19; CHAIN: A, C; CYCLIN A/CDK2-ASSOCIATED P45; CHAIN: B, D;	LIGASE SKP2 F-BOX; SKP1; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1606	1fs2	A	556	827	2.8e-42	-0.04	0.22		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1606	1ft8	A	622	769	0.0029	-0.04	0.03		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RIBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
1606	1i84		S280	367	2.8e-08	0.04	-0.19		SMOOTH MUSCLE MYOSIN HEAVY CHAIN; CHAIN: S, V; SMOOTH MUSCLE MYOSIN ESSENTIAL LIGHT CHAIN; CHAIN: T, W; SMOOTH MUSCLE MYOSIN REGULATORY LIGHT CHAIN; CHAIN: U, Z;	CONTRACTILE PROTEIN MYOSIN HEAVY CHAIN, GIZZARD SMOOTH MUSCLE; ELC, MYOSIN ALKALI LIGHT CHAIN; RLC, MYOSIN REGULATORY LIGHT CHAIN 2, SMOOTH MUSCLE PROTEIN, SMOOTH MUSCLE, MYOSIN SUBFRAGMENT 2, HEAVY 2 MEROMYOSIN, ESSENTIAL LIGHT CHAIN, REGULATORY LIGHT CHAIN, 3 MOTOR PROTEIN, COILED-COIL
1606	1yrg	A	616	837	1.4e-06	0.00	0.45		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1606	1yrg	A	624	817	2.4e-10	0.15	0.47		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TWINNING, MEROHEDRY TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1606	2bnh		571	823	1.3e-16	0.44	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1606	2bnh		622	797	1.2e-18	0.46	1.00		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1612	1fnf		31	454	1.4e-42			71.47	FIBRONECTIN; 1FNF 6 CHAIN: NULL; 1FNF 7	CELL ADHESION PROTEIN RGD, EXTRACELLULAR MATRIX 1FNF 18
1613	1cvj	A	55	235	1.4e-38			51.11	POLYDENYLATE BINDING PROTEIN 1; CHAIN: A, B, C, D, E, F, G, H; RNA (5'-R(*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3')]; CHAIN: M, N, O, P, Q, R, S, T;	GENE REGULATION/RNA POLY(A) BINDING PROTEIN 1, PABP 1; RRM, PROTEIN-RNA COMPLEX, GENE REGULATION/RNA
1613	1ha1		144	238	4.8e-29	0.80	1.00		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1613	1ha1		144	279	1.4e-59			110.55	HNRNP A1; CHAIN: NULL;	RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1613	1ha1		4	91	4.2e-36			72.80	HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1613	1ha1		53	224	1.4e-59	0.19	0.24		HNRNP A1; CHAIN: NULL;	NUCLEAR PROTEIN HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1, NUCLEAR PROTEIN, HNRNP, RBD, RRM, RNP, RNA BINDING, 2 RIBONUCLEOPROTEIN
1613	2up1	A	143	279	4.2e-62			105.46	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1613	2up1	A	3	91	4.2e-38			66.13	HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1613	2up1	A	52	230	4.2e-62	0.13	-0.01		CHAIN: B; HETEROGENEOUS NUCLEAR RIBONUCLEOPROTEIN A1; CHAIN: A; 12-NUCLEOTIDE SINGLE-STRANDED TELOMETRIC DNA; CHAIN: B;	COMPLEX (RIBONUCLEOPROTEIN/DNA) HNRNP A1, UP1; COMPLEX (RIBONUCLEOPROTEIN/DNA), HETEROGENEOUS NUCLEAR 2 RIBONUCLEOPROTEIN A1
1614	1by2		2	109	2.8e-44			108.34	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1614	1by2		38	150	1.4e-44			109.85	MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1614	1by2		41	146	1.4e-44	1.35	1.00		MAC-2 BINDING PROTEIN; CHAIN: NULL;	EXTRACELLULAR MODULE TUMOR-ASSOCIATED ANTIGEN 90K; EXTRACELLULAR MODULE, SCAVENGER RECEPTOR, TUMOUR-ASSOCIATED 2 ANTIGEN, EXTRACELLULAR MATRIX, GLYCOSYLATED PROTEIN
1614	1f5y	A	2	88	4.2e-23			51.72	LOW-DENSITY LIPOPROTEIN	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1614	1fyv	A	1	161	5.6e-51			98.94	RECEPTOR; CHAIN: A; TOLL-LIKE RECEPTOR 1; CHAIN: A;	HELIX, CALCIUM BINDING SIGNALING PROTEIN BETA-ALPHA-BETA FOLD PARALLEL BETA SHEET
1614	1fyx	A	5	154	2.8e-44			87.69	TOLL-LIKE RECEPTOR 2; CHAIN: A;	SIGNALING PROTEIN BETA-ALPHA-BETA FOLD
1616	1c1g	A	159	417	7.2e-11	-0.01	0.31		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1616	1c1g	A	159	443	7.2e-11			90.49	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1616	1c1g	A	373	417	0.00056	-0.45	0.12		TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1616	1dan	L	32	114	5.6e-09	0.01	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1616	1e7a	A	203	417	1.2e-08	-0.27	0.11		SERUM ALBUMIN; CHAIN: A, B;	CARRIER PROTEIN CARRIER PROTEIN, ALBUMIN, GENERAL ANESTHETIC, PROPOFOL
1616	1f5y	A	30	108	2.8e-12	0.17	-0.14		LOW-DENSITY LIPOPROTEIN RECEPTOR; CHAIN: A;	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10 HELIX, CALCIUM BINDING
1616	1f5y	A	37	107	2.4e-13	0.41	-0.12		LOW-DENSITY LIPOPROTEIN	LIPID BINDING PROTEIN LDL RECEPTOR; BETA HAIRPIN, 3-10

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1616	1hci	A	159	417	1.2e-10	0.01	0.58		RECEPTOR; CHAIN: A; ALPHA-ACTININ 2; CHAIN: A, B;	HELIX, CALCIUM BINDING TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
1616	1hci	A	321	416	0.00096	0.16	0.18		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-BINDING PROTEIN
1616	1hj7	A	35	115	7e-09	0.05	-0.20		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1616	2trc	P	301	350	0.0011	0.38	-0.07		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33; PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION)
1618	1sro		352	430	1.4e-22	0.39	1.00		PNPASE; CHAIN: NULL;	S1 RNA-BINDING DOMAIN POLYRIBONUCLEOTIDE NUCLEOTIDYLTRANSFERASE, S1 RNA-BINDING DOMAIN, POLYNUCLEOTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										PHOSPHORYLASE 2 (PNPASE)
1619	1a0j	A	30	226	4.2e-58	-0.08	0.93		TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1619	1a7s		30	252	2.8e-37			68.47	HEPARIN BINDING PROTEIN; CHAIN: NULL;	SERINE PROTEASE HOMOLOG CAP37, AZUROCIDIN, SERINE PROTEASE HOMOLOG, ENDOTOXIN BINDING, HEPARIN
1619	1d6w	A	7	122	8.4e-25	-0.20	0.55		THROMBIN; CHAIN: A; DECAPEPTIDE INHIBITOR; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR HYDROLASE, THROMBIN, THROMBIN INHIBITOR
1619	1ddj	A	12	266	7e-51			59.39	PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
1619	1dlk	B	30	230	8.4e-53	-0.29	0.53		DELTA-CHYMOTRYPSIN; CHAIN: A, C; DELTA-CHYMOTRYPSIN; CHAIN: B, D;	HYDROLASE DELTA-CHYMOTRYPSIN, PEPTIDIC INHIBIOR, CHLOROMETHYL KETONE
1619	1elt		30	263	4.2e-49			55.84	ELASTASE; 1ELT 4 CHAIN: NULL; 1ELT 5	SERINE PROTEINASE
1619	1elv	A	3	122	2.4e-24	-0.42	0.03		COMPLEMENT C1S COMPONENT; CHAIN: A;	HYDROLASE TRYPSIN-LIKE SERIN PROTEASE, CCP (OR SUSHI OR SCR)MODULE
1619	1ept	A	30	71	8.4e-19	-0.51	0.96		HYDROLASE (SERINE PROTEASE) PORCINE E-TRYPSIN (E.C.3.4.21.4) 1EPT 3	
1619	1euf	A	30	261	4.2e-49			59.76	DUODENASE; CHAIN: A;	HYDROLASE BOVINE DUODENASE, SERINE PROTEASE, DUAL SPECIFICITY, 2 CRYSTAL STRUCTURE
1619	1f7z	A	30	226	5.6e-55	-0.05	0.99		TRYPSIN II, ANIONIC;	HYDROLASE/HYDROLASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; PANCREATIC TRYPSIN INHIBITOR; CHAIN: I;	INHIBITOR BPTI SERINE PROTEASE, TRYPSIN PRECURSOR
1619	1fi8	A	30	221	1.3e-47	-0.15	0.39		NATURAL KILLER CELL PROTEASE 1; CHAIN: A, B; ECOTIN; CHAIN: C, E; ECOTIN; CHAIN: D, F;	HYDROLASE/HYDROLASE INHIBITOR GRANZYME B; COMPLEX (SERINE PROTEASE/INHIBITOR), PROTEASE SUBSTRATE 2 INTERACTIONS, BETA STRAND STRUCTURE, CHYMOTRYPSIN FOLD, 3 GRANZYME B, ECOTIN
1619	1fmi	A	30	226	1.4e-58	-0.05	0.81		TRYPSIN; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
1619	1fuj	A	30	255	5.6e-46			69.94	PR3; CHAIN: A, B, C, D;	HYDROLASE (SERINE PROTEASE) MYELOBLASTIN; HYDROLASE, SERINE PROTEASE, GLYCOPROTEIN, ZYMOGEN, SIGNAL
1619	1gct	A	30	230	1.1e-52	-0.08	0.21		HYDROLASE (SERINE PROTEINASE) GAMMA-*CHYMOTRYPSIN *A (E.C.3.4.21.1) ($P*H 7.0) 1GCT 3	
1619	1iau	A	30	266	5.6e-47			57.15	GRANZYME B; CHAIN: A; ACETYL-ISOLEUCYL-GLUTAMYL-PROLYL-ASPARTYL- CHAIN: B;	HYDROLASE ACE-ILE-GLU-PRO-ASP-CHO; HYDROLASE
1619	1pfx	C	30	241	1.3e-51	0.24	0.55		FACTOR IXA; CHAIN: C, L,; D-PHE-PRO-ARG; CHAIN: I;	COMPLEX (BLOOD COAGULATION/INHIBITOR) CHRISTMAS FACTOR; COMPLEX, INHIBITOR, HEMOPHILIA/EGF, BLOOD COAGULATION, 2 PLASMA, SERINE PROTEASE, CALCIUM-BINDING, HYDROLASE, 3 GLYCOPROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1619	1ppf	E	11	113	1.4e-32			75.05	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) (NEUTROPHIL ELASTASE (HNE)) 1PPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY 1PPF 4 OVOMUCOID INHIBITOR (OMTKY3) 1PPF 5	
1619	1ppf	E	30	233	1.3e-45			118.91	HYDROLASE(SERINE PROTEINASE) HUMAN LEUKOCYTE ELASTASE (HLE) (NEUTROPHIL ELASTASE (HNE)) 1PPF 3 (E.C.3.4.21.37) COMPLEX WITH THE THIRD DOMAIN OF TURKEY 1PPF 4 OVOMUCOID INHIBITOR (OMTKY3) 1PPF 5	
1619	1qnj	A	30	266	4.2e-46			55.54	ELASTASE; CHAIN: A;	HYDROLASE (SERINE PROTEASE) PPE; HYDROLASE(SERINE PROTEASE), ATOMIC RESOLUTION
1619	1slw	B	30	226	5.6e-56	0.07	0.71		ECOTIN; CHAIN: A; ANIONIC TRYPSIN; CHAIN: B;	COMPLEX (SERINE PROTEASE/INHIBITOR) TRYPSIN INHIBITOR; SERINE PROTEASE, INHIBITOR, COMPLEX, METAL BINDING SITES, 2 PROTEIN ENGINEERING, PROTEASE-SUBSTRATE INTERACTIONS, 3 METALLOPROTEINS
1619	1tm	A	30	226	4.2e-56	0.10	0.98		HYDROLASE (SERINE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEINASE) TRYPSIN (E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
1619	2sta	E	30	226	8.4e-60	0.03	0.92		TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: I	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
1619	5ptp		30	227	2.8e-53	-0.00	0.88		BETA TRYPSIN; CHAIN: NULL;	SERINE PROTEASE HYDROLASE, SERINE PROTEASE, DIGESTION, PANCREAS, 2 ZYMOGEN, SIGNAL
1620	1aui	A	1	191	5.6e-86			191.33	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1620	1aui	A	1	291	2.8e-99			289.74	SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1620	1aui	A	41	272	2.8e-99	0.41	1.00		SERINE/THREONINE PHOSPHATASE 2B; CHAIN: A, B;	HYDROLASE CALCINEURIN; HYDROLASE, PHOSPHATASE, IMMUNOSUPPRESSION
1620	1tco	A	1	191	5.6e-86			204.13	SERINE/THREONINE PHOSPHATASE B2; CHAIN: A, B; FK506-BINDING PROTEIN; CHAIN: C;	COMPLEX (HYDROLASE/ISOMERASE) CALCINEURIN A, CAM-PRP CATALYTIC SUBUNIT, FKBP-12, CIS-TRANS ISOMERASE; COMPLEX (HYDROLASE/ISOMERASE), IMMUNOSUPPRESSANT
1620	1tco	A	1	267	2.8e-98			290.51	SERINE/THREONINE PHOSPHATASE B2;	COMPLEX (HYDROLASE/ISOMERASE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
									CHAIN: A, B; FK506-BINDING PROTEIN; CHAIN: C;	CALCINEURIN A, CAM-PRP CATALYTIC SUBUNIT, FKBP-12, CIS-TRANS ISOMERASE; COMPLEX (HYDROLASE/ISOMERASE), IMMUNOSUPPRESSANT
1620	1tco	A	41	267	2.8e-98	0.31	1.00		SERINE/THREONINE PHOSPHATASE B2; CHAIN: A, B; FK506-BINDING PROTEIN; CHAIN: C;	COMPLEX (HYDROLASE/ISOMERASE) CALCINEURIN A, CAM-PRP CATALYTIC SUBUNIT, FKBP-12, CIS-TRANS ISOMERASE; COMPLEX (HYDROLASE/ISOMERASE), IMMUNOSUPPRESSANT
1625	1a7k	A	62	338	4.2e-25	-0.17	0.01		GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE; CHAIN: A, B, C, D;	OXIDOREDUCTASE GAPDH; GLYCERALDEHYDE-3-PHOSPHATE DEHYDROGENASE, GLYCOSOME, 2 TRYPANOSOME, OXIDOREDUCTASE
1625	1brm	A	1	192	7e-63			167.88	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE ASADH, ASDH; CRYSTAL STRUCTURE, DEHYDROGENASE, ESCHERICHIA COLI, ENZYME, 2 NADP
1625	1brm	A	2	308	0	0.50	1.00		ASPARTATE-SEMIALDEHYDE DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE ASADH, ASDH; CRYSTAL STRUCTURE, DEHYDROGENASE, ESCHERICHIA COLI, ENZYME, 2 NADP
1625	1brm	A	2	372	0			449.11	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE ASADH, ASDH; CRYSTAL STRUCTURE, DEHYDROGENASE, ESCHERICHIA COLI, ENZYME, 2 NADP
1625	1brm	A	3	129	1.4e-57			58.34	ASPARTATE-SEMIALDEHYDE DEHYDROGENASE; CHAIN: A, B, C;	OXIDOREDUCTASE ASADH, ASDH; CRYSTAL STRUCTURE, DEHYDROGENASE, ESCHERICHIA COLI, ENZYME, 2 NADP

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1626	1b7y	B	7	170	2.8e-43	0.10	1.00		PHENYLALANYL-TRNA SYNTHETASE; CHAIN: A; PHENYLALANYL-TRNA SYNTHETASE; CHAIN: B;	LIGASE PHERS; PHERS; ENZYME, TRNA SYNTHETASE, ALPHA/BETA HOMODIMER
1628	1b9m	A	28	97	0.00011	-0.87	0.19		MODE; CHAIN: A, B;	TRANSCRIPTION DNA-BINDING, GENE REGULATION, WINGED HELIX TURN HELIX, 2 MOLYBDATE, OB FOLD
1628	1b9m	A	8	97	0.00056	0.13	0.36		MODE; CHAIN: A, B;	TRANSCRIPTION DNA-BINDING, GENE REGULATION, WINGED HELIX TURN HELIX, 2 MOLYBDATE, OB FOLD
1628	1bi2	B	10	86	0.00014	-0.09	0.09		DIPHTHERIA TOXIN REPRESSOR; CHAIN: A, B;	REPRESSOR DTXR; REPRESSOR, TRANSCRIPTION REGULATION, DNA-BINDING, IRON
1628	1c0w	A	10	86	0.00014	-0.21	0.07		DIPHTHERIA TOXIN REPRESSOR; CHAIN: A, B, C, D; DNA (5'- CHAIN: E; DNA (5'- CHAIN: F;	GENE REGULATION/DNA IRON-DEPENDENT DIPHTHERIA TOX REGULATORY ELEMENT, TOXIN REPRESSOR-DNA COMPLEX, METAL BINDING SH-LIKE DOMAIN
1628	1ddn	A	10	86	0.00014	0.12	0.06		DIPHTHERIA TOX REPRESSOR; CHAIN: A, B, C, D; DIPHTHERIA TOX DNA OPERATOR; CHAIN: E, F;	COMPLEX (REGULATORY PROTEIN/DNA) DTXR; TOXPO; COMPLEX (REGULATORY PROTEIN/DNA), DIPHTHERIA TOX REPRESSOR, 2 TRANSCRIPTION REGULATION, DNA-BINDING REGULATORY PROTEIN, 3 IRON-REGULATED REPRESSOR, DNA-PROTEIN, DNA-REPRESSOR 4 COMPLEX
1628	2dtr		10	86	0.00014	-0.05	0.22		DIPHTHERIA TOXIN REPRESSOR; CHAIN: NULL;	REPRESSOR DTXR; TRANSCRIPTION REGULATION, REPRESSOR, DNA-BINDING, IRON

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1631	1nal	1	21	139	0.0048	-0.03	0.03		N-ACETYLNEURAMINATE LYASE; 1NAL 4 CHAIN: 1, 2, 3, 4; 1NAL 5	LYASE
1631	1zym	A	1	57	1.4e-12	-0.79	1.00		ENZYME I; CHAIN: A, B;	PHOSPHOTRANSFERASE PHOSPHOTRANSFERASE
1632	1a1s		263	599	0	0.20	0.86		ORNITHINE CARBAMOYLTRANSFERASE; CHAIN: NULL;	TRANSCARBAMYLASE ORNITHINE TRANSCARBAMYLASE; TRANSCARBAMYLASE
1632	1a1s		289	601	0			78.86	ORNITHINE CARBAMOYLTRANSFERASE; CHAIN: NULL;	TRANSCARBAMYLASE ORNITHINE TRANSCARBAMYLASE; TRANSCARBAMYLASE
1632	1duv	G	262	597	9.8e-85	0.08	0.31		ORNITHINE TRANSCARBAMOYLASE; CHAIN: G, H, I;	TRANSFERASE OCTASE-1; ENZYME-INHIBITOR COMPLEX
1632	1dxh	A	263	599	1.1e-85	-0.05	0.21		ORNITHINE CARBAMOYLTRANSFERASE; CHAIN: A;	TRANSFERASE ORNITHINE TRANSCARBAMYLASE; TRANSFERASE, TRANSCARBAMYLASE
1632	1dxh	A	402	585	9.6e-24	0.50	1.00		ORNITHINE CARBAMOYLTRANSFERASE; CHAIN: A;	TRANSFERASE ORNITHINE TRANSCARBAMYLASE; TRANSFERASE, TRANSCARBAMYLASE
1632	1oth	A	263	609	2.8e-93	-0.00	0.70		ORNITHINE TRANSCARBAMOYLASE; CHAIN: A;	TRANSFERASE TRANSCARBAMOYLASE, TRANSFERASE
1632	1oth	A	270	608	2.8e-93			75.53	ORNITHINE TRANSCARBAMOYLASE; CHAIN: A;	TRANSFERASE TRANSCARBAMOYLASE, TRANSFERASE
1632	2atc	A	262	598	4.2e-57	0.04	-0.09		TRANSFERASE (CARBAMOYL-P,ASPARTATE)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ASPARTATE CARBAMOYLTRANSFERASE (ASPARTATE TRANSCARBAMYLASE) 2ATC 4 (E.C.2.1.3.2) 2ATC 5	
1632	3csu	A	262	598	8.4e-61	0.21	0.11		ASPARTATE CARBAMOYLTRANSFERASE; CHAIN: A, B, C;	TRANSFERASE (CARBAMOYL-P, ASPARTATE) TRANSFERASE (CARBAMOYL-P, ASPARTATE)
1632	3csu	C	262	598	2.8e-67	-0.05	0.04		ASPARTATE CARBAMOYLTRANSFERASE; CHAIN: A, B, C;	TRANSFERASE (CARBAMOYL-P, ASPARTATE) TRANSFERASE (CARBAMOYL-P, ASPARTATE)
1634	1bk7	A	24	202	2.4e-16			54.70	RIBONUCLEASE MC1; CHAIN: A;	HYDROLASE RNASE MC1; HYDROLASE (NUCLEIC ACID, RNA)
1634	1bk7	A	78	138	2.4e-16	-0.11	0.06		RIBONUCLEASE MC1; CHAIN: A;	HYDROLASE RNASE MC1; HYDROLASE (NUCLEIC ACID, RNA)
1634	1dix	A	10	206	3.6e-17			59.98	EXTRACELLULAR RIBONUCLEASE LE; CHAIN: A;	HYDROLASE ALPHA PLUS BETA
1634	1dix	A	78	138	3.6e-17	0.13	0.55		EXTRACELLULAR RIBONUCLEASE LE; CHAIN: A;	HYDROLASE ALPHA PLUS BETA
1635	1c1g	A	70	346	7.2e-09			64.80	TROPOMYOSIN; CHAIN: A, B, C, D	CONTRACTILE PROTEIN TROPOMYOSIN COILED-COIL ALPHA-HELICAL, CONTRACTILE PROTEIN
1635	1hci	A	126	274	4.8e-09	-0.27	0.10		ALPHA-ACTININ 2; CHAIN: A, B;	TRIPLE-HELIX COILED COIL ALPHA ACTININ SKELETAL MUSCLE ISOFORM 2, TRIPLE-HELIX COILED COIL, CONTRACTILE PROTEIN, MUSCLE, 2 Z-LINE, ACTIN-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1638	1br1	B	32	176	1.2e-29			73.41	MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	BINDING PROTEIN MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1638	1br1	B	38	173	1.2e-29	0.16	1.00		MYOSIN; CHAIN: A, B, C, D, E, F, G, H;	MUSCLE PROTEIN MDE; MUSCLE PROTEIN
1638	1cll		30	174	6e-35			111.80	CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
1638	1cll		38	173	6e-35	0.06	1.00		CALCIUM-BINDING PROTEIN CALMODULIN (VERTEBRATE) 1CLL 3	
1638	1cmf		1	66	7e-34			51.56	CALMODULIN (VERTEBRATE); 1CMF 6 CHAIN: NULL; 1CMF 7	CALCIUM-BINDING PROTEIN CALMODULIN APO TR2C-DOMAIN; 1CMF 9
1638	1exr	A	28	173	1.2e-34			107.65	CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1638	1exr	A	38	173	1.2e-34	0.30	1.00		CALMODULIN; CHAIN: A;	METAL TRANSPORT CALMODULIN, HIGH RESOLUTION, DISORDER
1638	1fw4	A	1	63	1.4e-32			53.23	CALMODULIN; CHAIN: A;	METAL BINDING PROTEIN EF-HAND, HELIX-LOOP-HELIX, FRAGMENT, CALCIUM, TR2C, C- 2 TERMINAL DOMAIN, CALMODULIN
1638	1ggw	A	33	175	2.4e-08			73.80	CDC4P; CHAIN: A;	CYTOKINE EF-HAND PROTEIN, MYOSIN LIGHT CHAIN; LIGHT CHAIN, CYTOKINESIS, CELL CYCLE, EF-HAND
1638	1jf0	A	31	111	2.4e-11	0.61	0.95		OBELIN; CHAIN: A;	LUMINESCENT PROTEIN BIOLUMINESCENCE, CALCIUM-REGULATED PHOTOPROTEIN, OBELIN, 2 OBELIA, HYDROID
1638	1trc	A	1	65	2.8e-33			52.26	CALCIUM BINDING	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PROTEIN CALMODULIN (/TR=2=C$ FRAGMENT COMPRISING RESIDUES 78 - 148 1TRC 3 OF THE INTACT MOLECULE) 1TRC 4	
1638	1vrk	A	27	175	1.2e-34			110.08	CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1638	1vrk	A	38	173	1.2e-34	0.18	1.00		CALMODULIN; CHAIN: A; RS20; CHAIN: B;	CALMODULIN, CALCIUM BINDING, HELIX-LOOP-HELIX, SIGNALLING, 2 COMPLEX(CALCIUM-BINDING PROTEIN/PEPTIDE)
1643	1jj2	R	197	276	1.1e-32	0.53	0.99		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L6; CHAIN: E; RIBOSOMAL PROTEIN L7AE; CHAIN: F; RIBOSOMAL PROTEIN L10; CHAIN: G; RIBOSOMAL PROTEIN L10E; CHAIN: H; RIBOSOMAL PROTEIN	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10; 50S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN P0, HMAL10, L10E; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STRAT AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									L13; CHAIN: I; RIBOSOMAL PROTEIN L14; CHAIN: J; RIBOSOMAL PROTEIN L15; CHAIN: K; RIBOSOMAL PROTEIN L15E; CHAIN: L; RIBOSOMAL PROTEIN L18; CHAIN: M; RIBOSOMAL PROTEIN L18E; CHAIN: N; RIBOSOMAL PROTEIN L19E; CHAIN: O; RIBOSOMAL PROTEIN L21E; CHAIN: P; RIBOSOMAL PROTEIN L22; CHAIN: Q; RIBOSOMAL PROTEIN L23; CHAIN: R; RIBOSOMAL PROTEIN L24; CHAIN: S; RIBOSOMAL PROTEIN L24E; CHAIN: T; RIBOSOMAL PROTEIN L29; CHAIN: U; RIBOSOMAL PROTEIN L30; CHAIN: V; RIBOSOMAL PROTEIN L31E; CHAIN: W; RIBOSOMAL PROTEIN L32E; CHAIN: X; RIBOSOMAL PROTEIN L37AE; CHAIN: Y; RIBOSOMAL PROTEIN L37E; CHAIN: Z;	HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RIBOSOMAL PROTEIN L39E; CHAIN: 1; RIBOSOMAL PROTEIN L44E; CHAIN: 2;	
1643	1jj2	R	197	276	5.6e-27	0.53	0.99		23S RRNA; CHAIN: 0; 5S RRNA; CHAIN: 9; RIBOSOMAL PROTEIN L2; CHAIN: A; RIBOSOMAL PROTEIN L3; CHAIN: B; RIBOSOMAL PROTEIN L4; CHAIN: C; RIBOSOMAL PROTEIN L5; CHAIN: D; RIBOSOMAL PROTEIN L6; CHAIN: E; RIBOSOMAL PROTEIN L7AE; CHAIN: F; RIBOSOMAL PROTEIN L10; CHAIN: G; RIBOSOMAL PROTEIN L10E; CHAIN: H; RIBOSOMAL PROTEIN L13; CHAIN: I; RIBOSOMAL PROTEIN L14; CHAIN: J; RIBOSOMAL PROTEIN L15; CHAIN: K; RIBOSOMAL PROTEIN L15E; CHAIN: L; RIBOSOMAL PROTEIN L18; CHAIN: M; RIBOSOMAL PROTEIN L18E; CHAIN: N; RIBOSOMAL PROTEIN	RIBOSOME 50S RIBOSOMAL PROTEIN L2P, HMAL2, HL4; 50S RIBOSOMAL PROTEIN L3P, HMAL3, HL1; 50S RIBOSOMAL PROTEIN L4E, HMAL4, HL6; 50S RIBOSOMAL PROTEIN L5P, HMAL5, HL13; 50S RIBOSOMAL PROTEIN L6P, HMAL6, HL10; 50S RIBOSOMAL PROTEIN HS6; 50S RIBOSOMAL PROTEIN P0, HMAL10, L10E; 50S RIBOSOMAL PROTEIN L13P, HMAL13; 50S RIBOSOMAL PROTEIN L14P, HMAL14, HL27; 50S RIBOSOMAL PROTEIN L15P, HMAL15, HL9; 50S RIBOSOMAL PROTEIN L18P, HMAL18, HL12; 50S RIBOSOMAL PROTEIN L18E, HL29, L19; 50S RIBOSOMAL PROTEIN L19E, HMAL19, HL24; 50S RIBOSOMAL PROTEIN L21E, HL31; 50S RIBOSOMAL PROTEIN L22P, HMAL22, HL23; 50S RIBOSOMAL PROTEIN L23P, HMAL23, HL25, L21; 50S RIBOSOMAL PROTEIN L24P, HMAL24, HL16, HL15; 50S RIBOSOMAL PROTEIN L24E, HL21/HL22; 50S RIBOSOMAL PROTEIN L29P, HMAL29, HL33; 50S RIBOSOMAL PROTEIN L30P, HMAL30, HL20, HL16; 50S

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									L19E; CHAIN: O; RIBOSOMAL PROTEIN L21E; CHAIN: P; RIBOSOMAL PROTEIN L22; CHAIN: Q; RIBOSOMAL PROTEIN L23; CHAIN: R; RIBOSOMAL PROTEIN L24; CHAIN: S; RIBOSOMAL PROTEIN L24E; CHAIN: T; RIBOSOMAL PROTEIN L29; CHAIN: U; RIBOSOMAL PROTEIN L30; CHAIN: V; RIBOSOMAL PROTEIN L31E; CHAIN: W; RIBOSOMAL PROTEIN L32E; CHAIN: X; RIBOSOMAL PROTEIN L37AE; CHAIN: Y; RIBOSOMAL PROTEIN L37E; CHAIN: Z; RIBOSOMAL PROTEIN L39E; CHAIN: 1; RIBOSOMAL PROTEIN L44E; CHAIN: 2;	RIBOSOMAL PROTEIN L31E, L34, HL30; 50S RIBOSOMAL PROTEIN L32E, HL5; 50S RIBOSOMAL PROTEIN L37E, L35E; 50S RIBOSOMAL PROTEINS L39E, HL39E, HL46E; 50S RIBOSOMAL PROTEIN L44E, LA, HLA RIBOSOME ASSEMBLY, RNA-RNA, PROTEIN-RNA, PROTEIN-PROTEIN
1644	1qq4	A	141	313	8.4e-08	0.67	-0.11		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1644	1qq4	A	185	330	1.2e-06	0.46	-0.09		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1645	1ehd	A	680	767	2.8e-05	-0.01	0.06		AGGLUTININ ISOLECTIN VI; CHAIN: A	PLANT PROTEIN TWO HOMOLOGOUS HEVEIN-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										DOMAINS
1645	1emn		490	555	2.8e-09	0.03	-0.20		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1645	1emn		525	631	1.4e-07	0.62	-0.07		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1645	1emn		677	747	7e-09	0.19	-0.18		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1645	1fak	L	360	443	2.8e-09	0.02	-0.20		BLOOD COAGULATION FACTOR VIIA; CHAIN: L; BLOOD COAGULATION FACTOR VIIA; CHAIN: H; SOLUBLE TISSUE FACTOR; CHAIN: T; 5L15; CHAIN: I;	BLOOD CLOTTING COMPLEX(SERINE PROTEASE/COFACTOR/LIGAND), BLOOD COAGULATION, 2 SERINE PROTEASE, COMPLEX, CO-FACTOR, RECEPTOR ENZYME, 3 INHIBITOR, GLA, EGF, COMPLEX (SERINE 4 PROTEASE/COFACTOR/LIGAND), BLOOD CLOTTING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1645	1g44	A	570	755	2.4e-08	0.16	-0.19		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1645	1g44	C	404	630	4.8e-08	0.07	-0.17		COMPLEMENT CONTROL PROTEIN; CHAIN: A, B, C;	IMMUNE SYSTEM BETA, MODULE
1645	1igr	A	408	679	6e-09	0.33	-0.19		INSULIN-LIKE GROWTH FACTOR RECEPTOR 1; CHAIN: A;	HORMONE RECEPTOR HORMONE RECEPTOR, INSULIN RECEPTOR FAMILY
1645	1klo		363	523	2.8e-11	0.11	-0.19		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1645	1klo		403	555	5.6e-09	0.07	-0.20		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1645	1klo		469	624	1.4e-09	0.19	-0.18		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1645	1klo		532	676	4.2e-10	0.30	-0.17		LAMININ; CHAIN: NULL;	GLYCOPROTEIN GLYCOPROTEIN
1645	1skz		352	456	1.4e-08	0.08	-0.20		ANTISTASIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR FACTOR XA INHIBITOR; ANTISTASIN, CRYSTAL STRUCTURE, FACTOR XA INHIBITOR, 2 SERINE PROTEASE INHIBITOR, THROMBOSIS
1645	4mt2		434	488	5.6e-08	-0.00	-0.19		METALLOTHIONEIN METALLOTHIONEIN ISOFORM II 4MT2 3	
1645	9wga	A	337	497	1.4e-18	0.36	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1645	9wga	A	400	560	5.6e-18	0.24	-0.18		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1645	9wga	A	445	612	1.4e-17	0.28	-0.17		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1645	9wga	A	460	673	1.3e-16	0.30	-0.09		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1645	9wga	A	519	706	2.8e-15	0.16	-0.14		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1645	9wga	A	584	742	2.8e-17	0.47	-0.13		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1645	9wga	A	622	762	4.2e-15	0.26	-0.12		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1650	1ck4	A	8	253	5.6e-49			170.57	INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
1651	1aox	A	5	258	1.4e-44			145.63	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1651	1aox	A	83	337	8.4e-44			146.30	INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1651	1aox	A	84	335	8.4e-44	0.53	1.00		INTEGRIN ALPHA 2 BETA; CHAIN: A, B;	INTEGRIN INTEGRIN, CELL ADHESION, GLYCOPROTEIN
1651	1atz	A	272	331	2.4e-09	-0.39	0.07		VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
1651	1atz	A	86	268	3.6e-23			57.40	VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
1651	1atz	A	88	175	3.6e-23	0.35	0.93		VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1651	1atz	A	88	306	1.3e-16	0.07	0.63		VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
1651	1atz	A	8	191	2.8e-15			55.88	VON WILLEBRAND FACTOR; CHAIN: A, B;	COLLAGEN-BINDING COLLAGEN-BINDING, HEMOSTASIS, DINUCLEOTIDE BINDING FOLD
1651	1auq		1	228	4.2e-22			51.56	A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1651	1auq		69	306	7e-22			56.38	A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1651	1auq		84	342	7e-22	0.06	-0.02		A1 DOMAIN OF VON WILLEBRAND FACTOR; CHAIN: NULL;	WILLEBRAND WILLEBRAND, BLOOD COAGULATION, PLATELET, GLYCOPROTEIN
1651	1ck4	A	86	331	2.8e-48			170.36	INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
1651	1ck4	A	87	332	2.8e-48	0.71	1.00		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
1651	1dzi	A	244	323	1.2e-16	0.15	1.00		INTEGRIN; CHAIN: A; COLLAGEN; CHAIN: B, C, D;	INTEGRIN INTEGRIN, COLLAGEN
1651	1dzi	A	86	324	1.1e-38			120.10	INTEGRIN; CHAIN: A; COLLAGEN; CHAIN: B, C, D;	INTEGRIN INTEGRIN, COLLAGEN
1651	1dzi	A	88	174	1.2e-19	0.35	1.00		INTEGRIN; CHAIN: A; COLLAGEN; CHAIN: B, C, D;	INTEGRIN INTEGRIN, COLLAGEN
1651	1dzi	A	88	319	1.1e-38	0.40	1.00		INTEGRIN; CHAIN: A; COLLAGEN; CHAIN: B, C, D;	INTEGRIN INTEGRIN, COLLAGEN
1651	1dzi	A	8	246	2.8e-38			118.42	INTEGRIN; CHAIN: A;	INTEGRIN INTEGRIN, COLLAGEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									COLLAGEN; CHAIN: B, C, D;	
1651	1fns	A	233	337	7.2e-13	0.06	0.10		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
1651	1fns	A	6	197	2.8e-22			50.42	IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
1651	1fns	A	84	205	8.4e-22	0.42	0.46		IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
1651	1fns	A	84	275	8.4e-22			52.21	IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: L; IMMUNOGLOBULIN NMC-4 IGG1; CHAIN: H; VON WILLEBRAND FACTOR; CHAIN: A;	IMMUNE SYSTEM VON WILLEBRAND FACTOR, GLYCOPROTEIN IBA (A:ALPHA) BINDING, 2 COMPLEX (WILLEBRAND/IMMUNOGLOBULIN), BLOOD COAGULATION TYPE 3 2B VON WILLEBRAND DISEASE
1651	1ido		10	251	2.8e-38			55.95	INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										CYTOSKELETON
1651	1ido		88	329	5.6e-34			55.68	INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1651	1ido		89	329	5.6e-34	0.45	1.00		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN, EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1651	1lfa	A	88	334	7e-30	0.35	0.69		CD11A; 1LFA 5 CHAIN: A, B; 1LFA 6	CELL ADHESION LFA-1, ALPHA-L\BETA-2 INTEGRIN, A-DOMAIN; 1LFA 8
1651	1qc5	A	7	252	4.2e-48			163.00	ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1651	1qc5	A	85	330	9.8e-47	0.47	1.00		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1651	1qc5	A	85	330	9.8e-47			163.53	ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1652	1a14	H	1	93	1.4e-46			62.07	NEURAMINIDASE; CHAIN: N; SINGLE CHAIN ANTIBODY; CHAIN: H, L;	COMPLEX (ANTIBODY/ANTIGEN) COMPLEX (ANTIBODY/ANTIGEN), SINGLE-CHAIN ANTIBODY, 2 GLYCOSYLATED PROTEIN
1652	1a6v	H	1	94	1.4e-46			68.99	B1-8; CHAIN: L, H, M, I, N, J;	IMMUNOGLOBULIN IMMUNOGLOBULIN, HAPTEN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1652	1ay1	H	206	315	1.4e-55	0.36	0.84		TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCR, 2 HOT START
1652	1ay1	H	20	232	5.6e-55			150.59	TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCR, 2 HOT START
1652	1ay1	H	21	141	5.6e-55	0.70	1.00		TP7 FAB; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, FAB, ENZYME INHIBITOR, PCR, 2 HOT START
1652	1bf6	B	21	172	8.4e-35	0.44	0.69		CAMPATH-1G ANTIBODY; CHAIN: A, B, C, D, E, F, G, H;	ANTIBODY ANTIBODY, FAB, CAMPATH-1G, CD52
1652	1bvk	B	1	103	5.6e-46			113.70	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1652	1bvk	B	206	316	1.4e-56	0.56	0.94		HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1652	1bvk	B	20	135	1.3e-54			125.75	HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1652	1bvk	B	20	141	1.3e-54	0.59	1.00		HULYS11; CHAIN: A, B, D, E; LYSOZYME; CHAIN: C, F;	ANTIBODY/HYDROLASE) COMPLEX (HUMANIZED ANTIBODY/HYDROLASE) MURAMIDASE; HUMANIZED ANTIBODY, ANTIBODY COMPLEX, FV, ANTI-LYSOZYME, 2 COMPLEX (HUMANIZED ANTIBODY/HYDROLASE)
1652	1c12	B	20	231	1.4e-51			139.41	ANTIBODY FRAGMENT FAB; CHAIN: A; ANTIBODY FRAGMENT FAB; CHAIN: B;	IMMUNE SYSTEM ANTIBODY-ANTIGEN COMPLEX, SCFV FRAGMENT, CDRH3, MUSK 2 ODORANT, ODORANT SPECIFICITY, IMMUNE SYSTEM
1652	1c5d	B	20	257	7e-47			127.26	MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC CHAIN: L, A; MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC CHAIN: H, B;	IMMUNE SYSTEM IMMUNOGLOBULIN
1652	1c5d	B	21	172	7e-47	0.44	1.00		MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC CHAIN: L, A; MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC CHAIN: H, B;	IMMUNE SYSTEM IMMUNOGLOBULIN
1652	1ce1	H	206	316	4.2e-55	0.31	0.81		CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									PEPTIDE ANTIGEN; CHAIN: P;	
1652	1ce1	H	20	144	2.8e-54	0.81	1.00		CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1652	1ce1	H	20	224	2.8e-54			137.30	CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1652	1cf8	H	207	316	5.6e-55	0.59	0.94		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
1652	1cf8	H	21	147	2.8e-55	0.49	1.00		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
1652	1cl7	H	1	93	2.8e-37			71.49	IGG1 ANTIBODY 1696 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 1696 (VARIABLE HEAVY CHAIN); CHAIN: H; IGG1 ANTIBODY 1696 (CONSTANT HEAVY CHAIN); CHAIN: I;	IMMUNE SYSTEM IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1; IMMUNOGLOBULIN, IGG1 FAB FRAGMENT, CROSS-REACTIVITY, HIV1 PROTEASE, ENZYME 2 INHIBITION, IMMUNOGLOBULIN
1652	1clz	H	21	172	1.3e-33	0.38	0.34		IGG FAB (IGG3, KAPPA);	IMMUNOGLOBULIN MBR96 FAB

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: L, H;	(IMMUNOGLOBULIN); IMMUNOGLOBULIN C REGION, GLYCOPROTEIN, TRANSMEMBRANE
1652	1dby	A	12	122	1.4e-32			69.28	CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC THIOREDOXIN
1652	1dn0	B	206	316	1.4e-64	0.48	0.98		IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN); CHAIN: A, C; IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
1652	1dn0	B	20	240	5.6e-62			141.50	IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN); CHAIN: A, C; IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
1652	1dn0	B	21	144	5.6e-62	0.75	1.00		IGM-KAPPA COLD AGGLUTININ (LIGHT CHAIN); CHAIN: A, C; IGM-KAPPA COLD AGGLUTININ (HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM FAB, IGM, ANTIBODY, COLD AGGLUTININ, HUMAN
1652	1dqd	H	20	246	1.4e-51			131.91	FAB HGR-2 F6; CHAIN: L; FAB HGR-2 F6; CHAIN: H;	IMMUNE SYSTEM GLUCAGON RECEPTOR, MONOCLONAL ANTIBODY, FAB, RECEPTOR 2 ANTAGONIST, TYPICAL IMMUNOGLOBULIN FOLD, LIGHT CHAIN, HEAVY 3 CHAIN, ANTIGEN BINDING SITE, COMPLEMENTARITY-DETERMINING 4 REGIONS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1652	1eo8	H	20	258	1.2e-49	-0.09	0.21		HEMAGGLUTININ (HA1 CHAIN); CHAIN: A; HEMAGGLUTININ (HA2 CHAIN); CHAIN: B; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	VIRUS/VIRAL PROTEIN COMPLEX (HEMAGGLUTININ/IMMUNOGLOBULIN), HEMAGGLUTININ, 2 IMMUNOGLOBULIN, VIRAL PROTEIN, IMMUNE SYSTEM COMPLEX
1652	1ezv	X	20	124	2.4e-64	0.69	1.00		UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE CHAIN: A; UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CORE CHAIN: B; CYTOCHROME B; CHAIN: C; CYTOCHROME C1; CHAIN: D; UBIQUINOL-CYTOCHROME C REDUCTASE IRON-SULFUR CHAIN: E; UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 17 KD CHAIN: H; UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX 14 KD CHAIN: F; UBIQUINOL-CYTOCHROME C REDUCTASE COMPLEX CHAIN: G; UBIQUINOL-	OXIDOREDUCTASE/ELECTRON TRANSPORT CYTOCHROME BC1 COMPLEX, COMPLEX III, QCR, MITOCHONDRIA, 2 YEAST, ANTIBODY FV-FRAGMENT, STIGMATELLIN, COENZYME Q6, 3 MATRIX PROCESSING PEPTIDASES, UBIQUINONE, ELECTRON TRANSFER, 4 PROTON TRANSFER, Q-CYCLE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CYTOCHROME C REDUCTASE COMPLEX 7.3 KD CHAIN: I; HEAVY CHAIN (VH) OF FV-FRAGMENT; CHAIN: X; LIGHT CHAIN (VL) OF FV-FRAGMENT; CHAIN: Y;	
1652	1f11	B	20	258	3.6e-50	0.08	0.18		F124 IMMUNOGLOBULIN (KAPPA LIGHT CHAIN); CHAIN: A, C; F124 IMMUNOGLOBULIN (IGG1 HEAVY CHAIN); CHAIN: B, D;	IMMUNE SYSTEM IMMUNOGLOBULIN, ANTIBODY, FAB, HEPATITIS B, PRES2
1652	1f58	H	207	316	1.4e-54	0.43	0.98		IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1652	1f58	H	21	147	7e-55	0.58	1.00		IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1652	1f8t	H	207	316	4.2e-57	0.33	1.00		ANTIBODY FAB FRAGMENT (LIGHT CHAIN); CHAIN: L; ANTIBODY FAB	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING FRAGMENT, INTERLEUKIN- 2 2, X-RAY ANALYSIS, CRYSTAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FRAGMENT (HEAVY CHAIN); CHAIN: H	
1652	1f8t	H	21	147	4.2e-56	0.68	1.00		ANTIBODY FAB FRAGMENT (LIGHT CHAIN); CHAIN: L; ANTIBODY FAB FRAGMENT (HEAVY CHAIN); CHAIN: H	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING FRAGMENT, INTERLEUKIN- 2 2, X-RAY ANALYSIS, CRYSTAL
1652	1fb6	A	14	121	7e-33			68.84	THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1652	1h8n	A	21	296	7.2e-50	0.12	-0.08		MUTANT AL2 6E7S9G; CHAIN: A;	ANTIBODY ANTIBODY, FRAMEWORK
1652	1hi6	B	20	258	1.2e-47	-0.01	0.01		IGG2A KAPPA ANTIBODY CB41 (LIGHT CHAIN); CHAIN: A; IGG2A KAPPA ANTIBODY CB41 (HEAVY CHAIN); CHAIN: B; PEPTIDE 5; CHAIN: C;	COMPLEX (ANTIBODY/PEPTIDE) POLYSPECIFICITY, CROSSREACTIVITY, FAB-FRAGMENT, PEPTIDE, 2 HIV-1
1652	1ibg	H	21	229	7e-45	0.25	0.70		IMMUNOGLOBULIN IGG FAB (IGG2B, KAPPA) FRAGMENT (40-50 FAB) COMPLEXED WITH 1IBG 3 OUABAIN 1IBG 4	
1652	1ic7	H	21	117	1.2e-61	0.71	1.00		LYSOZYME BINDING IG KAPPA CHAIN; CHAIN: L; IGG1 FAB CHAIN H; CHAIN: H; LYSOZYME C; CHAIN: Y;	PROTEIN BINDING/HYDROLASE ANTIGEN-ANTIBODY COMPLEX, HYHEL-10, ANTI-HEN EGG WHITE 2 LYSOZYME ANTIBODY
1652	1jhl	H	1	93	2.8e-44			63.09	COMPLEX(ANTIBODY-ANTIGEN) FV FRAGMENT (IGG1, KAPPA) (LIGHT AND HEAVY VARIABLE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									DOMAINS 1JHL 3 NON-COVALENTLY ASSOCIATED) OF MONOCLONAL ANTI-HEN EGG 1JHL 4 LYSOZYME ANTIBODY D11.15 COMPLEX WITH PHEASANT EGG 1JHL 5 LYSOZYME 1JHL 6	
1652	1jth	H	21	127	6e-56	0.89	1.00		ANTIBODY A6; CHAIN: L, H; INTERFERON-GAMMA RECEPTOR ALPHA CHAIN; CHAIN: I;	COMPLEX (ANTIBODY/ANTIGEN) CYTOKINE RECEPTOR, COMPLEX (ANTIBODY/ANTIGEN), 2 TRANSMEMBRANE, GLYCOPROTEIN
1652	1mco	H	209	316	2.8e-55	0.45	0.82		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1652	1mek		7	125	5.6e-32			99.63	PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM
1652	1nsn	H	20	239	1.4e-49			142.58	IGG FAB (IGG1, KAPPA); 1NSN 4 CHAIN: L, H; 1NSN 5 STAPHYLOCOCCAL NUCLEASE; 1NSN 9 CHAIN: S; 1NSN 10	COMPLEX (IMMUNOGLOBULIN/HYDROLASE) N10 FAB IMMUNOGLOBULIN; 1NSN 7 STAPHYLOCOCCAL NUCLEASE RIBONUCLEATE; 1NSN 11 IMMUNOGLOBULIN, STAPHYLOCOCCAL NUCLEASE 1NSN 25
1652	1osp	H	20	240	2.8e-45			136.38	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSPA; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEI

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										N), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1, BORRELIA BURGDORFERI 3 STRAIN B31
1652	1qkz	H	21	172	2.8e-34	0.36	0.53		ANTIBODY; CHAIN: H, L; PROTEIN G-PRIME; CHAIN: A; MAJOR OUTER MEMBRANE PROTEIN P1.16; CHAIN: P;	IMMUNE SYSTEM FAB, PORA, NEISSERIA MENINGITIDIS, PORIN
1652	1sm3	H	20	172	2.8e-34	0.45	0.47		SM3 ANTIBODY; CHAIN: L, H; PEPTIDE EPITOPE; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE EPITOPE) ANTIBODY, PEPTIDE ANTIGEN, ANTITUMOR ANTIBODY, 2 COMPLEX (ANTIBODY/PEPTIDE EPITOPE)
1652	2trx	A	11	126	2.8e-33			80.58	ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2TRXA 3	
1652	32c2	B	207	316	5.6e-55	0.49	0.99		IGG1 ANTIBODY 32C2; CHAIN: A; IGG1 ANTIBODY 32C2; CHAIN: B;	IMMUNE SYSTEM FAB, ANTIBODY, AROMATASE, P450
1652	7fab	H	1	104	2.8e-46			78.15	IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
1652	7fab	H	207	316	4.2e-54	0.24	0.99		IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	
1652	7fab	H	20	224	1.3e-52			158.83	IMMUNOGLOBULIN FAB' NEW (LAMBDA LIGHT CHAIN) 7FAB 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1658	1a0r	P	389	562	9.6e-30	0.12	-0.17		TRANSDUCIN; CHAIN: B, G; PHOSDUCIN; CHAIN: P;	COMPLEX (TRANSDUCER/TRANSDUCTION) GT BETA-GAMMA; MEKA, PP33 PHOSDUCIN, TRANSDUCIN, BETA-GAMMA, SIGNAL TRANSDUCTION, 2 REGULATION, PHOSPHORYLATION, G PROTEINS, THIOREDOXIN, 3 VISION, MEKA, COMPLEX (TRANSDUCER/TRANSDUCTION), 4 POST-TRANSLATIONAL MODIFICATION, FARNESYL, FARNESYLATION HEADER HETNAM
1658	1a8l		324	560	5.6e-15	0.14	0.25		PROTEIN DISULFIDE OXIDOREDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, PDI, THIOREDOXIN FOLD
1658	1a8l		338	570	1.1e-41	0.31	0.78		PROTEIN DISULFIDE OXIDOREDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, PDI, THIOREDOXIN FOLD
1658	1a8l		463	690	7e-20	0.20	0.10		PROTEIN DISULFIDE OXIDOREDUCTASE; CHAIN: NULL;	OXIDOREDUCTASE OXIDOREDUCTASE, PDI, THIOREDOXIN FOLD
1658	1a8y		319	689	2.8e-19	0.24	0.09		CALSEQUESTRIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTRIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
1658	1a8y		321	630	1.2e-39	0.08	0.90		CALSEQUESTRIN; CHAIN: NULL	CALCIUM-BINDING PROTEIN CALSEQUESTRIN, CALCIUM-BINDING PROTEIN, SARCOPLASMIC 2 RETICULUM, RABBIT SKELETAL MUSCLE
1658	1cqg	A	462	554	1.4e-22	0.34	0.99		THIOREDOXIN; CHAIN: A; REF-1 PEPTIDE;	COMPLEX (ELECTRON TRANSPORT/PEPTIDE) COMPLEX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1658	1cqg	A	575	688	9.8e-20	0.21	-0.09		CHAIN: B; THIOREDOXIN; CHAIN: A; REF-1 PEPTIDE;	ELECTRON TRANSPORT/PEPTIDE COMPLEX (ELECTRON TRANSPORT/PEPTIDE) COMPLEX,
1658	1dby	A	13	119	8.4e-26			66.72	CHAIN: B; CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	ELECTRON TRANSPORT/PEPTIDE OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC
1658	1dby	A	326	431	6e-29	0.77	1.00		CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	THIOREDOXIN OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC
1658	1dby	A	330	432	2.8e-25	0.93	1.00		CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	THIOREDOXIN OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC
1658	1dby	A	461	570	4.8e-30	0.61	1.00		CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	THIOREDOXIN OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC
1658	1dby	A	465	568	8.4e-26	0.60	1.00		CHLOROPLAST THIOREDOXIN M CH2; CHAIN: A;	THIOREDOXIN OXIDOREDUCTASE THIOREDOXIN M, THIOREDOXIN CH2, CHLOROPLASTIC
1658	1erv		462	554	5.6e-25	0.39	0.96		THIOREDOXIN; CHAIN: NULL;	THIOREDOXIN OXIDOREDUCTASE DIMER, THIOREDOXIN, X-RAY CRYSTALLOGRAPHY, OXIDOREDUCTASE
1658	1f9m	A	7	119	2.8e-18			56.09	THIOREDOXIN F; CHAIN: A, B;	ELECTRON TRANSPORT
1658	1faa	A	1	119	2.8e-18			55.11	THIOREDOXIN F; CHAIN: A;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1658	1fb6	A	14	118	1.4e-27			67.56	THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1658	1fb6	A	327	431	1.4e-26	0.85	1.00		THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1658	1fb6	A	327	431	2.4e-28	0.85	1.00		THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1658	1fb6	A	462	563	1.1e-29	0.22	1.00		THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1658	1fb6	A	462	568	7e-27	0.17	1.00		THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1658	1fb6	A	578	689	1.3e-23	0.47	-0.05		THIOREDOXIN M; CHAIN: A, B;	ELECTRON TRANSPORT ELECTRON TRANSPORT
1658	1mek		321	435	2.8e-26	0.50	0.83		PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM
1658	1mek		322	431	2.4e-26	0.82	1.00		PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM
1658	1mek		455	573	2.4e-28			99.73	PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM
1658	1mek		457	562	2.4e-28	1.03	1.00		PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM
1658	1mek		587	687	1.4e-18	0.22	0.24		PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM
1658	1mek		6	122	8.4e-27			93.85	PROTEIN DISULFIDE ISOMERASE; CHAIN: NULL;	ELECTRON TRANSPORT ELECTRON TRANSPORT, REDOX-ACTIVE CENTER, ISOMERASE, 2 ENDOPLASMIC RETICULUM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1658	1quw	A	13	120	1.4e-24			61.41	THIOREDOXIN; CHAIN: A;	ELECTRON TRANSPORT ALPHA/BETA OPEN-TWISTED PROTEIN, THIOL-DISULFIDE
1658	1quw	A	327	432	9.6e-27	0.91	1.00		THIOREDOXIN; CHAIN: A;	ELECTRON TRANSPORT ALPHA/BETA OPEN-TWISTED PROTEIN, THIOL-DISULFIDE
1658	1quw	A	465	558	4.2e-26	0.44	1.00		THIOREDOXIN; CHAIN: A;	ELECTRON TRANSPORT ALPHA/BETA OPEN-TWISTED PROTEIN, THIOL-DISULFIDE
1658	1quw	A	594	689	1.1e-22	0.28	-0.12		THIOREDOXIN; CHAIN: A;	ELECTRON TRANSPORT ALPHA/BETA OPEN-TWISTED PROTEIN, THIOL-DISULFIDE
1658	1thx		11	119	1.1e-22			64.88	THIOREDOXIN; 1THX 5 CHAIN: NULL; 1THX 6	ELECTRON TRANSPORT THIOREDOXIN 2; 1THX 7 OXIDO-REDUCTASE 1THX 16
1658	1thx		324	431	3.6e-29	0.84	1.00		THIOREDOXIN; 1THX 5 CHAIN: NULL; 1THX 6	ELECTRON TRANSPORT THIOREDOXIN 2; 1THX 7 OXIDO-REDUCTASE 1THX 16
1658	1thx		575	689	8.4e-19	0.37	0.36		THIOREDOXIN; 1THX 5 CHAIN: NULL; 1THX 6	ELECTRON TRANSPORT THIOREDOXIN 2; 1THX 7 OXIDO-REDUCTASE 1THX 16
1658	2trx	A	11	116	9.8e-28			75.24	ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
1658	2trx	A	324	431	4.8e-30	0.94	1.00		ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
1658	2trx	A	324	431	8.4e-27	1.06	1.00		ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
1658	2trx	A	461	563	7.2e-30	0.43	1.00		ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
1658	2trx	A	462	565	8.4e-27	0.37	1.00		ELECTRON TRANSPORT	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1658	2trx	A	575	690	2.8e-24	0.45	0.15		THIOREDOXIN 2TRXA 2 2TRXA 3 ELECTRON TRANSPORT THIOREDOXIN 2TRXA 2 2TRXA 3	
1662	1c3p	A	1134	1434	1.4e-69	0.31	0.98		HDLP (HISTONE DEACETYLASE-LIKE PROTEIN); CHAIN: A;	LYASE ALPHA/BETA FOLD, LYASE
1666	1en2	A	31	113	1.4e-06	0.17	-0.02		AGGLUTININ ISOLECTIN I/AGGLUTININ ISOLECTIN V// CHAIN: A;	SUGAR BINDING PROTEIN UDA; LECTIN, HEVEIN DOMAIN, UDA, SUPERANTIGEN, SACCHARIDE BINDING
1666	2rel		11	67	8.4e-23			111.70	R-ELAFIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R-ELAFIN, ELASTASE INHIBITOR
1666	2rel		61	117	4.8e-24	-0.64	1.00		R-ELAFIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R-ELAFIN, ELASTASE INHIBITOR
1666	2rel		61	117	4.8e-24			111.59	R-ELAFIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R-ELAFIN, ELASTASE INHIBITOR
1666	2rel		62	116	1.4e-11	-0.45	1.00		R-ELAFIN; CHAIN: NULL;	SERINE PROTEASE INHIBITOR SERINE PROTEASE INHIBITOR, R-ELAFIN, ELASTASE INHIBITOR
1672	1bih	A	132	426	2.8e-24	0.23	0.23		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1672	1bih	A	20	410	4.2e-46	0.11	-0.11		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1672	1bih	A	30	422	4.2e-46			96.50	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1672	1cdy		140	310	3.6e-20	0.26	0.24		T-CELL SURFACE	T-CELL SURFACE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									GLYCOPROTEIN CD4; CHAIN: NULL;	GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1672	1cs6	A	20	422	1.4e-59	0.30	0.78		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1672	1cs6	A	25	405	1.4e-59			104.76	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1672	1cvs	C	126	300	8.4e-29	0.01	0.35		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1672	1cvs	C	224	421	2.8e-41	0.35	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1672	1cvs	C	328	441	1.4e-15	0.05	-0.19		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1672	1cvs	D	124	310	9.8e-30			65.66	FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: C, D;	DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1672	1cvs	D	126	300	9.8e-30	0.10	0.96		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1672	1cvs	D	224	421	1.4e-37	0.42	0.69		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1672	1epf	A	132	310	3.6e-23	0.44	0.34		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1672	1epf	A	137	294	2.8e-19	0.22	0.86		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1672	1epf	A	21	202	7e-20	0.18	-0.17		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1672	1epf	A	235	421	1.4e-17	0.30	-0.03		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1672	1ev2	E	130	300	1.4e-24	-0.00	0.45		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E,	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									F, G, H;	DOMAINS, B-TREFOIL FOLD
1672	1ev2	E	226	421	1.1e-34	0.32	-0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1ev2	E	328	438	7e-15	0.00	-0.20		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1ev2	G	125	311	2.4e-23	0.25	0.96		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1ev2	G	226	425	1.1e-36	0.18	0.01		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1evt	C	122	311	1.3e-29			72.46	FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1evt	C	126	300	1.3e-29	0.00	1.00		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: C, D;	SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1evt	C	224	421	1.4e-35	0.54	-0.11		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1672	1f2q	A	138	293	4.2e-17	0.13	0.47		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1672	1f2q	A	20	223	1.4e-17	0.22	0.94		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1672	1f6a	A	130	293	5.6e-17	0.25	0.99		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1672	1f6a	A	16	223	1.1e-17	0.05	0.09		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1672	1f97	A	238	420	1.4e-22	0.25	0.12		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1672	1f97	A	27	215	1.4e-34	0.32	-0.11		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1672	1fcg	A	128	293	4.2e-15	0.20	0.98		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1672	1fcg	A	22	219	1.2e-18	-0.05	0.01		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1672	1fcg	A	247	421	1.2e-15	-0.25	0.03		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1672	1fhg	A	227	300	2.8e-13	0.16	0.16		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1672	1fnl	A	22	219	3.6e-18	-0.06	0.03		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1672	1fnl	A	240	421	2.4e-15	0.25	-0.08		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1672	1gl0x	A	130	297	4.8e-22	0.19	0.93		LEUCOCYTE IMMUNOGLOBULIN-LIKE RECEPTOR-1; CHAIN: A;	IMMUNE SYSTEM LEUKOCYTE INHIBITORY RECEPTOR-1; LEUKOCYTE IMMUNOGLOBULIN FOLD, 3-10 HELIX
1672	1iam		139	310	1.2e-14	0.00	0.07		INTERCELLULAR ADHESION MOLECULE-1; CHAIN: NULL;	RHINOVIRUS RECEPTOR ICAM-1, CD54; RHINOVIRUS RECEPTOR, CELL ADHESION, INTEGRIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										LIGAND, 2 GLYCOPROTEIN, LFA-1 LIGAND, IMMUNOGLOBULIN FOLD, 3 TRANSMEMBRANE
1672	1ie5	A	215	311	4.8e-13	-0.22	0.25		NEURAL CELL ADHESION MOLECULE; CHAIN: A;	CELL ADHESION N-CAM; INTERMEDIATE
1672	1igt	B	5	437	1.4e-10			79.51	IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN FOLD IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1672	1iil	G	226	425	2.8e-41	0.38	0.21		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1672	1iil	G	31	223	2.8e-26	0.11	-0.14		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1672	1itb	B	134	428	4.2e-29			69.34	INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1672	1itb	B	151	419	4.2e-29	0.02	0.17		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1672	1itb	B	24	310	1.2e-24	0.16	0.17		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR) COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1672	1nkr		131	313	1.2e-17			70.67	P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1672	1nkr		133	297	1.2e-17	0.05	0.82		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1672	1nkr		23	219	1.2e-16	0.21	0.00		P58-CL42 KIR; CHAIN: NULL;	INHIBITORY RECEPTOR KILLER CELL INHIBITORY RECEPTOR; INHIBITORY RECEPTOR, NATURAL KILLER CELLS, IMMUNOLOGICAL 2 RECEPTORS, IMMUNOGLOBULIN FOLD
1672	1vca	A	242	353	2.4e-13	-0.04	0.01		HUMAN VASCULAR CELL ADHESION MOLECULE-1; IVCA 4 CHAIN: A, B; IVCA 5	CELL ADHESION PROTEIN VCAM-D1,2; IVCA 6 IMMUNOGLOBULIN SUPERFAMILY, INTEGRIN-BINDING IVCA 15
1672	1wio	A	27	410	1.2e-27			92.72	T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1672	1wio	A	27	417	1.2e-27	0.04	-0.14		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	LIPOPROTEIN, POLYMORPHISM GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1672	2dli	A	131	316	1.2e-22			66.58	MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1672	2dli	A	133	312	1.2e-22	0.20	0.82		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1672	2dli	A	23	219	6e-19	0.14	-0.09		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1672	2fcb	A	128	293	1.4e-15	0.29	0.68		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1672	2fcb	A	247	421	2.4e-15	0.07	0.04		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1672	8fab	A	25	211	5.6e-17	0.21	-0.14		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1673	1a25	A	507	632	7e-27	0.32	0.47		PROTEIN KINASE C	CALCIUM-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									(BETA); CHAIN: A, B;	CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1673	1byn	A	502	630	1.4e-27	0.12	0.95		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1673	1djx	A	491	619	5.6e-20	0.05	-0.15		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3 PHOSPHOINOSITIDE-SPECIFIC
1673	1dqv	A	500	646	2.8e-29	0.21	0.90		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1673	1dsy	A	507	632	1.3e-26	-0.05	0.42		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
1673	1rsy		497	627	2.8e-27	0.25	0.93		CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1673	3rpb	A	522	639	7e-25	0.08	0.04		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1678	1ao7	E	22	154	2.8e-42	0.05	0.88		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA-A2 HEAVY CHAIN; CLASS I MHC, T-CELL RECEPTOR, VIRAL PEPTIDE, 2 COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR
1678	1bd2	E	22	154	9.8e-44	-0.05	0.48		HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1678	1becc		23	154	1.4e-41	-0.03	0.51		14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5 CHAIN: NULL; 1BEC 6	RECEPTOR T CELL RECEPTOR 1BEC 14
1678	1bj1	J	20	158	5.6e-43	0.00	-0.19		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1678	1d9k	B	22	136	1.4e-40			53.60	T-CELL RECEPTOR D10 (ALPHA CHAIN); CHAIN: A, E; T-CELL RECEPTOR D10 (BETA CHAIN); CHAIN: B, F; MHC I-AK A CHAIN (ALPHA CHAIN); CHAIN: C, G; MHC I-AK B CHAIN (BETA CHAIN);	IMMUNE SYSTEM MHC I-AK; MHC I-AK; T-CELL RECEPTOR, MHC CLASS II, D10, I-AK

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: D, H; CONALBUMIN PEPTIDE; CHAIN: P, Q;	
1678	1dee	A	20	158	8.4e-43	0.17	-0.19		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
1678	1fgv	L	20	153	8.4e-42	0.20	-0.14		IMMUNOGLOBULIN FV FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 1FGV 3 ANTIBODY 'H52' (HUH52-AA FV) 1FGV 4	
1684	1edo	A	3	261	4.5e-73			58.51	BETA-KETO ACYL CARRIER PROTEIN REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NUCLEOTIDE FOLD, ROSSMANN FOLD
1684	1edo	A	5	233	4.5e-73	0.52	-0.20		BETA-KETO ACYL CARRIER PROTEIN REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NUCLEOTIDE FOLD, ROSSMANN FOLD
1684	1fds		2	241	6e-73	0.75	-0.20		17-BETA-HYDROXYSTEROID-DEHYDROGENASE; CHAIN: NULL;	DEHYDROGENASE DEHYDROGENASE, 17-BETA-HYDROXYSTEROID
1684	1fds		2	242	6e-73			304.79	17-BETA-HYDROXYSTEROID-DEHYDROGENASE; CHAIN: NULL;	DEHYDROGENASE DEHYDROGENASE, 17-BETA-HYDROXYSTEROID
1685	1erg		132	212	0.00053	0.03	-0.20		COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN CD59 (EXTRACELLULAR 1ERG 3 REGION,	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	
1685	1erg		24	107	0.0018	0.08	-0.20		COMPLEMENT FACTOR HUMAN COMPLEMENT REGULATORY PROTEIN CD59 (EXTRACELLULAR 1ERG 3 REGION, RESIDUES 1 - 70) (NMR, RESTRAINED MINIMIZED 1ERG 4 AVERAGE STRUCTURE) 1ERG 5	
1686	1b6c	B	1	238	3e-75			127.53	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1686	1b6c	B	523	908	1.5e-97			202.68	FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE KINASE
1686	1b6c	B	526	907	1.5e-97	0.37	-0.20		FK506-BINDING PROTEIN; CHAIN: A, C, E, G; TGF-B SUPERFAMILY RECEPTOR TYPE I; CHAIN: B, D, F, H;	COMPLEX (ISOMERASE/PROTEIN KINASE) FKBP12; SERINE/THREONINE-PROTEIN KINASE RECEPTOR R4; COMPLEX (ISOMERASE/PROTEIN KINASE), RECEPTOR 2 SERINE/THREONINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										KINASE
1686	1blx	A	559	852	3e-28	0.18	-0.20		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1686	1byg	A	551	772	9e-32	0.08	-0.20		C-TERMINAL SRC KINASE; CHAIN: A;	TRANSFERASE CSK; PROTEIN KINASE, C-TERMINAL SRC KINASE, PHOSPHORYLATION, 2 STAUROSPORINE, TRANSFERASE
1686	1e1x	A	552	770	9e-30	0.23	-0.20		CYCLIN-DEPENDENT PROTEIN KINASE 2; CHAIN: A;	PROTEIN KINASE CDK2; PROTEIN KINASE, CELL CYCLE, PHOSPHORYLATION, CELL DIVISION, 2 MITOSIS, INHIBITION
1686	1f3m	C	557	772	1.3e-28	0.24	-0.20		SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: A, B; SERINE/THREONINE-PROTEIN KINASE PAK-ALPHA; CHAIN: C, D;	TRANSFERASE KINASE DOMAIN, AUTOINHIBITORY FRAGMENT, HOMODIMER
1686	1fgk	A	553	770	1.8e-32	0.15	-0.20		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR, PHOSPHOTRANSFERASE
1686	1fgk	A	575	843	3e-32	0.17	-0.20		FGF RECEPTOR 1; CHAIN: A, B;	PHOSPHOTRANSFERASE FGFR1K, FIBROBLAST GROWTH FACTOR RECEPTOR 1; TRANSFERASE, TYROSINE-PROTEIN KINASE, ATP-BINDING, 2 PHOSPHORYLATION, RECEPTOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOL D score	Compound	PDB annotation
1686	1fmk		553	836	3e-38	0.06	-0.20		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE,
1686	1hcl		552	770	1.5e-30	0.02	-0.20		HUMAN CYCLIN-DEPENDENT KINASE 2; CHAIN: NULL;	PHOSPHOTRANSFERASE PROTEIN KINASE CDK2; TRANSFERASE, SERINE/THREONINE PROTEIN KINASE, ATP-BINDING, 2 CELL CYCLE, CELL DIVISION, MITOSIS, PHOSPHORYLATION
1686	1i44	A	552	843	9e-30	0.16	-0.20		INSULIN RECEPTOR; CHAIN: A;	TRANSFERASE IR; PROTEIN TYROSINE KINASE, PHOSPHOTRANSFERASE
1686	1i44	A	553	770	2.4e-30	0.14	-0.20		INSULIN RECEPTOR; CHAIN: A;	TRANSFERASE IR; PROTEIN TYROSINE KINASE, PHOSPHOTRANSFERASE
1686	1iep	A	553	842	3e-38	0.08	-0.20		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE ABL; CHAIN: A, B;	TRANSFERASE P150, C-ABL; KINASE, KINASE INHIBITOR, STI-571, ACTIVATION LOOP
1686	1ir3	A	552	843	3e-31	0.17	-0.20		INSULIN RECEPTOR; CHAIN: A; PEPTIDE SUBSTRATE; CHAIN: B;	COMPLEX (TRANSFERASE/SUBSTRATE) TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1686	1ir3	A	553	770	5.9e-33	0.40	-0.20		INSULIN RECEPTOR; CHAIN: A; PEPTIDE	COMPLEX (TRANSFERASE/SUBSTRATE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									SUBSTRATE; CHAIN: B;	TYROSINE KINASE, SIGNAL TRANSDUCTION, PHOSPHOTRANSFERASE, 2 COMPLEX (KINASE/PEPTIDE SUBSTRATE/ATP ANALOG), ENZYME, 3 COMPLEX (TRANSFERASE/SUBSTRATE)
1686	1phk		552	772	1.1e-30	0.27	-0.20		PHOSPHORYLASE KINASE; CHAIN: NULL;	KINASE RABBIT MUSCLE PHOSPHORYLASE KINASE; GLYCOGEN METABOLISM, TRANSFERASE, SERINE/THREONINE-PROTEIN, 2 KINASE, ATP-BINDING, CALMODULIN-BINDING
1686	1qcf	A	553	836	3e-33	0.04	-0.20		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1686	1vr2	A	553	770	4.7e-32	0.11	-0.20		VASCULAR ENDOTHELIAL GROWTH FACTOR RECEPTOR CHAIN: A;	TRANSFERASE KDR; TYROSINE KINASE
1688	1fmk		149	233	2.9e-29	0.04	-0.20		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1688	1fmk		149	233	4.5e-26	0.04	-0.20		TYROSINE-PROTEIN KINASE SRC; CHAIN: NULL;	PHOSPHOTRANSFERASE C-SRC, P60-SRC; SRC, TYROSINE KINASE, PHOSPHORYLATION, SH2, SH3, 2 PHOSPHOTYROSINE, PROTO-ONCOGENE, PHOSPHOTRANSFERASE
1688	1fyn	A	146	207	2.4e-18			82.54	PHOSPHOTRANSFERASE	TRANSFERASE PROTO-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FYN; CHAIN: A; 3BP-2; CHAIN: B;	ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTID E)
1688	1fyn	A	148	207	2.4e-18	0.53	-0.20		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTID E)
1688	1fyn	A	7	68	1.5e-21			86.38	PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTID E)
1688	1g2b	A	137	188	1.8e-14	0.22	-0.20		SPECTRIN ALPHA CHAIN; CHAIN: A;	METAL BINDING PROTEIN CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, SH3 2 DOMAIN, CYTOSKELETON
1688	1g83	A	150	233	1.2e-16	0.08	-0.20		PROTO-ONCOGENE TYROSINE-PROTEIN	TRANSFERASE P59-FYN; BETA BARREL, ANTIPARALLEL BETA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									KINASE FYN; CHAIN: A, B;	SHEET, ALPHA HELIX, 3-10 2 HELIX
1688	1g83	A	150	233	3e-29			73.74	PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN; CHAIN: A, B;	TRANSFERASE P59-FYN; BETA BARREL, ANTIPARALLEL BETA SHEET, ALPHA HELIX, 3-10 2 HELIX
1688	1g83	A	152	233	3e-29	0.47	-0.20		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN; CHAIN: A, B;	TRANSFERASE P59-FYN; BETA BARREL, ANTIPARALLEL BETA SHEET, ALPHA HELIX, 3-10 2 HELIX
1688	1gri	A	6	208	3e-05			50.90	GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1688	1iij	A	131	213	1.2e-15	0.07	-0.20		MELANOMA DERIVED GROWTH REGULATORY PROTEIN; CHAIN: A, B;	HORMONE/GROWTH FACTOR MELANOMA INHIBITORY ACTIVITY; SH3 SUBDOMAIN
1688	1qcf	A	148	233	2.4e-32	0.01	-0.20		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2 ORDERED ACTIVATION LOOP
1688	1shf	A	10	68	3e-21			83.69	PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1688	1shf	A	149	207	1.2e-18	0.28	-0.20		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1688	1shf	A	149	207	1.2e-18			79.90	PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									(SH3 DOMAIN) 1SHF 4	
1688	1tud		137	188	1.2e-14	0.37	-0.20		ALPHA-SPECTRIN; CHAIN: NULL;	CYTOSKELETON CAPPING PROTEIN, CALCIUM-BINDING, DUPLICATION, REPEAT, 2 SH3 DOMAIN, CYTOSKELETON
1693	1a4y	A	506	751	5.9e-30	0.19	-0.20		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1693	1a9n	A	492	587	1.2e-14	0.15	-0.20		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1a9n	A	511	671	1.2e-22	0.07	-0.20		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1a9n	A	619	749	1.2e-16	0.32	-0.20		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1a9n	A	669	760	3e-09	0.17	-0.20		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1a9n	C	494	624	3.5e-17	0.32	-0.20		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1a9n	C	511	702	2.4e-19	0.10	-0.20		U2 RNA HAIRPIN IV;	COMPLEX (NUCLEAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1693	1a9n	C	619	749	5.9e-17	0.23	-0.20		CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1a9n	C	664	760	3.5e-09	0.21	-0.20		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1693	1d0b	A	481	640	3e-14	0.22	-0.20		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1693	1d0b	A	490	642	5.9e-18	0.15	-0.20		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1693	1d0b	A	504	696	5.3e-20	0.02	-0.20		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1693	1d0b	A	514	747	1.8e-23	0.10	-0.20		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1693	1d0b	A	525	673	4.5e-16	0.41	-0.20		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1693	1ds9	A	613	749	1.2e-13	0.13	-0.20		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1693	1fs2	A	527	750	5.9e-12	0.20	-0.20		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1693	1jvr		396	433	0.0012	0.04	-0.20		HUMAN T-CELL LEUKEMIA VIRUS TYPE II MATRIX CHAIN: NULL;	MATRIX PROTEIN HTLV-II MA, MA; HUMAN T-CELL LEUKEMIA VIRUS TYPE II MATRIX PROTEIN, HTLV-II 2 MATRIX PROTEIN, HTLV-II MA, RETROVIRAL MATRIX PROTEIN, P17
1693	1yrg	A	503	750	4.1e-28	0.15	-0.20		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1693	2bnh		504	749	3.5e-32	0.34	-0.20		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1694	1cka	A	124	170	0.001	0.23	-0.20		COMPLEX (ONCOGENE PROTEIN/PEPTIDE) C-CRK (N-TERMINAL SH3 DOMAIN) (C-CRKSH3-N) COMPLEXED WITH 1CKA 3 C3G PEPTIDE (PRO-PRO-PRO-ALA-LEU-PRO-PRO-LYS-LYS-ARG) 1CKA 4	
1694	1cka	A	19	73	1e-12	0.12	-0.20		COMPLEX (ONCOGENE PROTEIN/PEPTIDE) C-CRK (N-TERMINAL SH3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									DOMAIN) (C-CRKSH3-N) COMPLEXED WITH 1CKA 3 C3G PEPTIDE (PRO-PRO-PRO-ALA-LEU-PRO-PRO-LYS-LYS-ARG) 1CKA 4	
1694	1efn	A	21	70	6e-13	0.14	-0.20		FYN TYROSINE KINASE; CHAIN: A, C; HIV-1 NEF PROTEIN; CHAIN: B, D;	COMPLEX (SH3 DOMAIN/VIRAL ENHANCER) SRC-HOMOLOGY 3 DOMAIN; COMPLEX (SH3 DOMAIN/VIRAL ENHANCER), PROTO-ONCOGENE, 2 TRANSFERASE, TYROSINE-PROTEIN KINASE, PHOSPHORYLATION, 3 AIDS, MYRISTYLATION, GTP-BINDING, ATP-BINDING, SH3 DOMAIN, 4 SH2 DOMAIN, PPII HELIX, PXYP MOTIF
1694	1fyn	A	17	70	4.5e-14	0.36	-0.20		PHOSPHOTRANSFERASE FYN; CHAIN: A; 3BP-2; CHAIN: B;	TRANSFERASE PROTO-ONCOGENE TYROSINE KINASE; PROTO-ONCOGENE, TRANSFERASE, TYROSINE-PROTEIN KINASE, 2 PHOSPHORYLATION, ATP-BINDING, MYRISTYLATION, SH3 DOMAIN, 3 COMPLEX (PHOSPHOTRANSFERASE/PEPTIDE)
1694	1g83	A	21	80	6e-14	0.20	-0.20		PROTO-ONCOGENE TYROSINE-PROTEIN KINASE FYN; CHAIN: A, B;	TRANSFERASE P59-FYN; BETA BARREL, ANTIPARALLEL BETA SHEET, ALPHA HELIX, 3-10 2 HELIX
1694	1gbq	A	21	74	4.5e-12	0.33	-0.20		GRB2; CHAIN: A; SOS-1; CHAIN: B;	COMPLEX (SIGNAL TRANSDUCTION/PEPTIDE) COMPLEX (SIGNAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1694	1gbr	A	123	176	0.001	0.31	-0.20		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	TRANSDUCTION/PEPTIDE), SH3 DOMAIN
1694	1gbr	A	21	82	1.3e-12	0.28	-0.20		SIGNAL TRANSDUCTION PROTEIN GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL 1GBR 3 SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE 1GBR 4 (NMR, 29 STRUCTURES) 1GBR 5	
1694	1gcq	A	125	173	1.5e-07	0.40	-0.20		GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; CHAIN: A, B; VAV PROTO-ONCOGENE; CHAIN: C;	SIGNALING PROTEIN/SIGNALING PROTEIN SH3 DOMAIN, PROTEIN-PROTEIN COMPLEX, GRB2,VAV
1694	1gcq	A	20	70	1.5e-14	0.24	-0.20		GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; CHAIN: A, B; VAV PROTO-ONCOGENE; CHAIN: C;	SIGNALING PROTEIN/SIGNALING PROTEIN SH3 DOMAIN, PROTEIN-PROTEIN COMPLEX, GRB2,VAV
1694	1gcq	B	125	173	1.5e-07	0.05	-0.20		GROWTH FACTOR	SIGNALING PROTEIN/SIGNALING

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RECEPTOR-BOUND PROTEIN 2; CHAIN: A, B; VAV PROTO-ONCOGENE; CHAIN: C;	PROTEIN SH3 DOMAIN, PROTEIN-PROTEIN COMPLEX, GRB2, VAV
1694	1gcq	B	20	70	1.5e-14	0.13	-0.20		GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2; CHAIN: A, B; VAV PROTO-ONCOGENE; CHAIN: C;	SIGNALING PROTEIN/SIGNALING PROTEIN SH3 DOMAIN, PROTEIN-PROTEIN COMPLEX, GRB2, VAV
1694	1gfc		17	70	1.3e-14	0.30	-0.20		ADAPTOR PROTEIN CONTAINING SH2 AND SH3 GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2) 1GFC 3 (C-TERMINAL SH3 DOMAIN) (NMR, MINIMIZED MEAN STRUCTURE) 1GFC 4	
1694	1gri	A	15	70	4.5e-15	0.16	-0.20		GROWTH FACTOR BOUND PROTEIN 2; 1GRI 5 CHAIN: A, B; 1GRI 6	SIGNAL TRANSDUCTION ADAPTOR SH2, SH3 1GRI 14
1694	1hsq		21	82	4.5e-12	0.21	-0.20		PHOSPHORIC DIESTER HYDROLASE PHOSPHOLIPASE C-GAMMA (SH3 DOMAIN) (E.C.3.1.4.11) 1HSQ 3 (NMR, MINIMIZED MEAN STRUCTURE) 1HSQ 4	
1694	1pwt		17	70	1.5e-12	0.55	-0.20		ALPHA SPECTRIN; CHAIN: NULL;	CIRCULAR PERMUTANT PWT; CIRCULAR PERMUTANT, SH3 DOMAIN, CYTOSKELETON
1694	1qcf	A	21	80	1.5e-11	0.28	-0.20		HAEMATOPOETIC CELL KINASE (HCK); CHAIN: A;	TYROSINE KINASE TYROSINE KINASE-INHIBITOR COMPLEX, DOWN-REGULATED KINASE, 2

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1694	1sem	A	19	73	1.5e-15	0.12	-0.20		SEM-5; 1SEM 3 CHAIN: A, B; 1SEM 5 10-RESIDUE PROLINE-RICH PEPTIDE FROM MSOS 1SEM 8 CHAIN: C, D 1SEM 10	ORDERED ACTIVATION LOOP SIGNAL TRANSDUCTION PROTEIN SRC-HOMOLOGY 3 (SH3) DOMAIN, PEPTIDE-BINDING PROTEIN, 1SEM 18 2 GUANINE NUCLEOTIDE EXCHANGE FACTOR 1SEM 19
1694	1shf	A	18	70	6e-14	0.36	-0.20		PHOSPHOTRANSFERASE FYN PROTO-ONCOGENE TYROSINE KINASE (E.C.2.7.1.112) 1SHF 3 (SH3 DOMAIN) 1SHF 4	
1694	1ycs	B	23	74	6e-12	0.34	-0.20		P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1694	2abl		13	80	4.5e-10	0.44	-0.20		ABL TYROSINE KINASE; CHAIN: NULL;	TRANSFERASE TRANSFERASE, TYROSINE KINASE, SH3, SH2, ONCOPROTEIN
1695	1jvr		180	216	0.0024	0.05	-0.20		HUMAN T-CELL LEUKEMIA VIRUS TYPE II MATRIX CHAIN: NULL;	MATRIX PROTEIN HTLV-II MA, MA; HUMAN T-CELL LEUKEMIA VIRUS TYPE II MATRIX PROTEIN, HTLV-II 2 MATRIX PROTEIN, HTLV-II MA, RETROVIRAL MATRIX PROTEIN, P17
1706	1a4y	A	647	870	5.9e-24	0.61	0.62		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE),

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1706	1a4y	A	669	956	4.5e-21	0.38	0.63		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1706	1a4y	A	684	869	2.4e-25	0.64	1.00		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1706	1a5e		370	490	1.2e-27	0.36	1.00		TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1706	1awc	B	353	503	1.2e-39	0.59	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1706	1awc	B	386	529	6e-36	0.23	1.00		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									1; CHAIN: B; DNA; CHAIN: D, E;	(TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1706	1awc	B	661	808	7.5e-11	0.34	-0.18		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1706	1awc	B	736	885	3e-24	0.13	-0.17		GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1706	1b3u	A	135	338	0.00012	0.19	-0.05		PROTEIN PHOSPHATASE PP2A; CHAIN: A, B;	SCAFFOLD PROTEIN SCAFFOLD PROTEIN, PP2A, PHOSPHORYLATION, HEAT REPEAT
1706	1bd8		346	470	7.5e-25	0.37	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1706	1bd8		356	506	1.5e-31	0.21	1.00		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1706	1bd8		389	548	4.5e-25	0.21	0.76		P19INK4D CDK4/6	TUMOR SUPPRESSOR TUMOR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									INHIBITOR; CHAIN: NULL;	SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1706	1bd8		419	574	1.5e-22	0.01	0.18		P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1706	1bi7	B	370	471	5.9e-25	0.37	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1706	1blx	B	346	470	4.5e-24	0.19	1.00		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1706	1blx	B	356	506	1.5e-30	0.29	0.99		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1706	1blx	B	389	535	6e-24	0.43	0.87		CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1706	1bu9	A	345	475	7.5e-27	0.38	0.88		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE,
1706	1bu9	A	353	508	1.2e-37	0.48	0.80		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE,
1706	1bu9	A	386	550	3e-30	0.25	0.60		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE,
1706	1bu9	A	422	574	1.2e-26	0.04	-0.08		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE,
1706	1d0b	A	697	870	5.9e-10	0.01	-0.03		INTERNALIN B; CHAIN: A;	HORMONE/GROWTH FACTOR CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1706	1d9s	A	376	488	1.8e-31	0.37	0.94		CYCLIN-DEPENDENT KINASE 4 INHIBITOR B; CHAIN: A;	SIGNALING PROTEIN HELIX-TURN-HELIX, ANKYRIN REPEAT
1706	1dcq	A	375	478	3e-28	0.21	1.00		PYK2-ASSOCIATED PROTEIN BETA; CHAIN: A;	METAL BINDING PROTEIN ZINC-BINDING MODULE, ANKYRIN REPEATS, METAL BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1706	1elr	A	150	253	1.8e-05	0.11	0.06		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1706	1elr	A	169	300	3.5e-09	-0.13	0.21		TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD; CHAIN: B;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN BINDING
1706	1feh	A	166	262	1.5e-05	-0.11	0.66		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1706	1feh	A	6	345	3.5e-14	0.07	0.15		PEROXISOMAL TARGETING SIGNAL 1 RECEPTOR; CHAIN: A, B; PTS1-CONTAINING PEPTIDE; CHAIN: C, D;	SIGNALING PROTEIN PEROXISMORE RECEPTOR 1, PTS1-BP, PEROXIN-5, PTS1 PROTEIN-PEPTIDE COMPLEX, TETRATRICOPEPTIDE REPEAT, TPR, 2 HELICAL REPEAT
1706	1fqv	A	632	869	5.9e-14	0.35	-0.03		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1706	1fs2	A	646	869	4.1e-12	0.27	0.11		SKP2; CHAIN: A, C; SKP1; CHAIN: B, D;	LIGASE CYCLIN A/CDK2-ASSOCIATED P45; CYCLIN A/CDK2-ASSOCIATED P19; SKP1, SKP2, F-BOX, LRRS, LEUCINE-RICH REPEATS, SCF, 2 UBIQUITIN, E3, UBIQUITIN PROTEIN LIGASE
1706	1ihb	A	345	474	3e-26	0.53	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A, B;	INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1706	1ihb	A	353	507	6e-37	0.39	1.00		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1706	1ihb	A	386	549	1.5e-29	0.15	0.74		CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6), ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1706	1ihg	A	171	273	5.9e-06	-0.09	0.60		CYCLOPHILIN 40; CHAIN: A;	ISOMERASE 40 KDA PEPTIDYL-PROLYL CIS-TRANS ISOMERASE; PPIASE IMMUNOPHILIN TETRATRICOPEPTIDE
1706	1ikn	D	348	511	4.5e-42	0.30	1.00		NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1706	1myo		353	472	1.2e-24	0.62	0.98		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1706	1myo		383	489	1.8e-33	0.61	-1202.08		MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1706	1nfi	E	347	511	7.5e-42	0.42	1.00		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1706	1nfi	E	380	565	9e-34	0.24	0.27		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT),
1706	1nfi	E	412	574	1.5e-28	-0.02	0.16		NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	ANKYRIN 2 REPEAT HELIX COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1706	1yrg	A	690	870	4.1e-24	0.90	-1202.08		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1706	2bnh		620	949	1.8e-26	0.40	-1202.08		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1706	2bnh		669	967	7.5e-22	0.35	0.90		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1708	1a1h	A	201	285	1.5e-30			70.74	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1708	1a1h	A	9	83	3e-29			65.50	QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1708	1ard		203	231	9e-07	0.03	-0.20		TRANSCRIPTION REGULATION YEAST TRANSCRIPTION FACTOR ADR1 (RESIDUES 102 - 130) 1ARD 3 (AMINO TERMINAL ZINC FINGER DOMAIN) (NMR, 10 STRUCTURES) 1ARD 4 (ADR1B) 1ARD 5	
1708	1mey	C	10	83	1.5e-44			70.07	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1708	1mey	C	12	90	4.5e-39			51.68	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1708	1mey	C	202	284	3e-47			76.62	DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1708	1mey	G	198	227	3e-11	0.36	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1708	1ubd	C	179	284	1.5e-33			74.99	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (ZINC FINGER/DNA) COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1708	1ubd	C	1	83	6e-29			59.28	YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1708	2adr		11	68	1.3e-07			53.15	ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1708	2gli	A	147	285	6e-32			65.93	ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1710	1b2w	L	1252	1288	0.0047	0.36	-0.20		ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNE SYSTEM IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
1710	1bec		1249	1289	0.0035	0.13	-0.20		14.3.D T CELL ANTIGEN RECEPTOR; 1BEC 5	RECEPTOR T CELL RECEPTOR 1BEC 14

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: NULL; 1BEC 6	
1710	1fyt	E	1252	1288	0.0059	0.24	-0.20		HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR CHAIN: A; HLA CLASS II HISTOCOMPATIBILITY ANTIGEN, DR-1 CHAIN: B; HEMAGGLUTININ HA1 PEPTIDE CHAIN; CHAIN: C; T-CELL RECEPTOR ALPHA CHAIN; CHAIN: D; T-CELL RECEPTOR BETA CHAIN; CHAIN: E;	IMMUNE SYSTEM HLA-DR1, DRA; HLA-DR1, DRB1 0101; TCR HA1.7 ALPHA CHAIN; TCR HA1.7 BETA CHAIN; PROTEIN-PROTEIN COMPLEX, IMMUNOGLOBULIN FOLD
1710	1hoc	A	1251	1289	0.0059	0.02	-0.20		HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D=B=, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1710	1qho	A	614	706	0.003	0.45	-0.20		ALPHA-AMYLASE; CHAIN: A;	HYDROLASE "MALTOGENIC" ALPHA AMYLASE; AMYLASE, GLYCOSIDE HYDROLASE, STARCH DEGRADATION
1711	1acp		182	260	2.9e-07			56.22	FATTY ACID SYNTHESIS PROTEIN ACYL CARRIER PROTEIN (NMR, 2 STRUCTURES) 1ACP 3	
1711	1acp		220	260	2.9e-07	0.21	-0.20		FATTY ACID SYNTHESIS PROTEIN ACYL CARRIER PROTEIN	

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Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									(NMR, 2 STRUCTURES) 1ACP 3	
1712	1boe	A	74	116	1.2e-17	0.33	-0.20		INSULIN-LIKE GROWTH FACTOR-BINDING PROTEIN-5 CHAIN: A;	HORMONE/GROWTH FACTOR MINI-IGFBP-5 MINI-IGFBP-5, IGFBP-5, IGF, INSULIN-LIKE GROWTH FACTOR 2 BINDING PROTEIN, NMR, HORMONE/GROWTH FACTOR
1712	1icf	I	262	331	4.5e-17	0.02	-0.20		CATHEPSIN L: HEAVY CHAIN; CHAIN: A, C; CATHEPSIN L: LIGHT CHAIN; CHAIN: B, D; INVARIANT CHAIN; CHAIN: I, J;	HYDROLASE II FRAGMENT, CD74 FRAGMENT CYSTEINE PROTEINASE, CATHEPSIN, MHC CLASS II, INVARIANT 2 CHAIN, THYROGLOBULIN TYPE-1 DOMAIN
1712	1mhu		90	117	0.0016	0.03	-0.20		METALLOTHIONEIN CD-7 METALLOTHIONEIN-2 (ALPHA DOMAIN) (/NMR$) 1MHUA 2	
1712	9wga	A	26	114	1.1e-11	0.03	-0.20		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1715	1c0t	A	4	226	0	0.08	-0.20		HIV-1 REVERSE TRANSCRIPTASE (A-CHAIN); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (B-CHAIN); CHAIN: B;	TRANSFERASE HIV-1 REVERSE TRANSCRIPTASE, AIDS, NON-NUCLEOSIDE INHIBITOR, 2 DRUG DESIGN
1715	1c9r	A	4	225	1.5e-99	0.22	-0.20		HIV-1 REVERSE TRANSCRIPTASE (CHAIN A); CHAIN: A; HIV-1 REVERSE TRANSCRIPTASE (CHAIN B); CHAIN: B; ANTIBODY (LIGHT	TRANSFERASE/IMMUNE SYSTEM/DNA HIV-1 RT; HIV-1 RT; HIV, REVERSE TRANSCRIPTASE, MET184ILE, 3TC, PROTEIN-DNA 2 COMPLEX, DRUG RESISTANCE, M184I, TRANSFERASE/IMMUNE 3 SYSTEM/DNA

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H; DNA (5'- CHAIN: T; DNA (5'- CHAIN: P;	
1715	1har		18	129	3e-61	0.02	-0.20		REVERSE TRANSCRIPTASE HIV-1 REVERSE TRANSCRIPTASE (AMINO-TERMINAL HALF) (FINGERS 1HAR 3 AND PALM SUBDOMAINS) (RT216) (E.C.2.7.49) 1HAR 4	
1715	1vrt	A	4	226	0	0.02	-0.20		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1715	1vrt	B	6	226	0	0.03	-0.20		HIV-1 REVERSE TRANSCRIPTASE; 1VRT 4 CHAIN: A, B; 1VRT 5	NUCLEOTIDYLTRANSFERASE HIV-1 RT; 1VRT 6 HIV-1 REVERSE TRANSCRIPTASE 1VRT 15
1718	1dkx	A	222	253	0.0059	0.63	-0.20		SUBSTRATE BINDING DOMAIN OF DNAK; CHAIN: A; SUBSTRATE PEPTIDE (7 RESIDUES); CHAIN: B;	COMPLEX (MOLECULAR CHAPERONE/PEPTIDE) DNAK, HEAT SHOCK PROTEIN 70 KDA (HSP70), COMPLEX 2 (MOLECULAR CHAPERONE/PEPTIDE)
1718	1e3p	A	222	264	0.00041	0.24	-0.20		GUANOSINE PENTAPHOSPHATE SYNTHETASE; CHAIN: A;	POLYRIBONUCLEOTIDE TRANSFERASE POLYNUCLEOTIDE PHOSPHORYLASE, GUANOSINE POLYRIBONUCLEOTIDE TRANSFERASE, ATP-GTP DIPHOSPHOTRANSFERASE, 2 RNA PROCESSING, RNA DEGRADATION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1718	1edh	A	363	544	3e-25	0.26	-0.20		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1718	1edh	A	373	544	1.2e-26	-0.00	-0.20		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1718	1edh	A	52	160	1.3e-18	0.19	-0.20		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1718	1edh	A	65	278	3e-51			88.39	E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1718	1efu	B	214	243	0.00041	0.35	-0.20		ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR TS; CHAIN: B, D;	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1718	1efu	B	220	267	0.0012	0.11	-0.20		ELONGATION FACTOR TU; CHAIN: A, C; ELONGATION FACTOR	COMPLEX (TWO ELONGATION FACTORS) ELONGATION FACTOR FOR TRANSFER, HEAT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									TS; CHAIN: B, D;	UNSTABLE, ELONGATION FACTOR FOR TRANSFER, HEAT STABLE, ELONGATION FACTOR, COMPLEX (TWO ELONGATION FACTORS)
1718	1g5z	A	217	243	0.0059	0.04	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1718	1g5z	A	218	243	0.0059	1.35	-0.20		OUTER SURFACE PROTEIN C; CHAIN: A;	IMMUNE SYSTEM SURFACE PROTEIN, ALPHA HELIX PROTEIN
1718	1ncg		63	158	3e-17	0.53	-0.20		N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN CADHERIN 1NCG 13
1718	1ncg		64	158	1.8e-28	0.45	-0.20		N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN CADHERIN 1NCG 13
1718	1ncg		6	101	7.5e-21			51.82	N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN CADHERIN 1NCG 13
1718	1nci	B	63	160	1.3e-16	0.61	-0.20		N-CADHERIN; 1NCI 3	CELL ADHESION PROTEIN CADHERIN 1NCI 13
1718	1nci	B	64	160	2.4e-27	0.38	-0.20		N-CADHERIN; 1NCI 3	CELL ADHESION PROTEIN CADHERIN 1NCI 13
1718	1ncj	A	370	544	3e-24	0.29	-0.20		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1718	1ncj	A	52	160	1.5e-16	0.21	-0.20		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1718	1ncj	A	64	285	1.5e-54			91.54	N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1718	1ncj	A	64	302	1.5e-54	0.05	-0.20		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL ADHESION PROTEIN
1718	1suh		63	164	9e-20	0.63	-0.20		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1718	1suh		64	163	5.9e-24	0.42	-0.20		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1718	1suh		6	107	1e-22			54.43	EPITHELIAL CADHERIN;	CELL ADHESION UVOMORULIN;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: NULL;	CADHERIN, CALCIUM BINDING, CELL ADHESION
1722	1bu7	A	110	531	4.2e-84	0.59	1.00		CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1722	1bu7	A	89	533	4.2e-84			185.73	CYTOCHROME P450; CHAIN: A, B;	OXIDOREDUCTASE FATTY ACID HYDROXYLASE; FATTY ACID MONOOXYGENASE, HEMOPROTEIN, P450 REMARK
1722	1cpt		110	530	5.6e-28	0.19	1.00		OXIDOREDUCTASE(OXYGENASE) CYTOCHROME P450-TERP 1CPT 3	
1722	1cpt		275	530	9.6e-40	0.06	0.69		OXIDOREDUCTASE(OXYGENASE) CYTOCHROME P450-TERP 1CPT 3	
1722	1cpt		92	531	5.6e-28			103.94	OXIDOREDUCTASE(OXYGENASE) CYTOCHROME P450-TERP 1CPT 3	
1722	1dt6	A	92	502	2.8e-74	0.22	1.00		CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYPIIC5 P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1722	1dt6	A	92	533	2.8e-74			140.71	CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYPIIC5 P450 1,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1722	1e9x	A	110	532	5.6e-76	0.61	1.00		CYTOCHROME P450 51-LIKE RV0764C; CHAIN: A;	OXIDOREDUCTASE CYP51, 14ALPHA-STEROL DEMETHYLASE; CYTOCHROME P450, 14 ALPHA-STEROL DEMETHYLASE, AZOLE 2 INHIBITORS
1722	1e9x	A	111	532	3.6e-94	0.72	1.00		CYTOCHROME P450 51-LIKE RV0764C; CHAIN: A;	OXIDOREDUCTASE CYP51, 14ALPHA-STEROL DEMETHYLASE; CYTOCHROME P450, 14 ALPHA-STEROL DEMETHYLASE, AZOLE 2 INHIBITORS
1722	1e9x	A	1	257	2.8e-45			79.09	CYTOCHROME P450 51-LIKE RV0764C; CHAIN: A;	OXIDOREDUCTASE CYP51, 14ALPHA-STEROL DEMETHYLASE; CYTOCHROME P450, 14 ALPHA-STEROL DEMETHYLASE, AZOLE 2 INHIBITORS
1722	1e9x	A	78	532	3.6e-94			308.79	CYTOCHROME P450 51-LIKE RV0764C; CHAIN: A;	OXIDOREDUCTASE CYP51, 14ALPHA-STEROL DEMETHYLASE; CYTOCHROME P450, 14 ALPHA-STEROL DEMETHYLASE, AZOLE 2 INHIBITORS
1722	1eup	A	122	501	1.2e-47	0.46	1.00		CYTOCHROME P450ERYF; CHAIN: A	OXIDOREDUCTASE CYTOCHROME P450, STEROID, ANDROSTENEDIONE, CYTOCHROME 2 P450ERYF
1722	1eup	A	124	500	7e-37	0.37	1.00		CYTOCHROME	OXIDOREDUCTASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									P450ERYF; CHAIN: A	CYTOCHROME P450, STEROID, ANDROSTENEDIONE,
1722	1eup	A	91	530	1.2e-47			108.69	CYTOCHROME P450ERYF; CHAIN: A	CYTOCHROME 2 P450ERYF OXIDOREDUCTASE CYTOCHROME P450, STEROID, ANDROSTENEDIONE, CYTOCHROME 2 P450ERYF
1722	1f24	A	106	526	4.8e-42			102.76	NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1722	1f24	A	122	498	4.8e-42	0.21	0.72		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1722	1f24	A	135	500	5.6e-21	0.16	1.00		NITRIC OXIDE REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NITRIC OXIDE REDUCTASE, CYTOCHROME P450NOR
1722	1fgx	A	8	318	0			342.49	BETA 1,4 GALACTOSYLTRANSFERASE; CHAIN: A, B;	TRANSFERASE BETA4GALT1; NUCLEOTIDE BINDING PROTEIN, ALPHA BETA ALPHA FOLD
1722	1fo3	A	1	278	2.8e-52			54.01	ALPHA1,2-MANNOSIDASE; CHAIN: A;	HYDROLASE ALPHA-ALPHA7 BARREL
1722	1io7	A	107	530	1.1e-19			88.39	CYTOCHROME P450 CYP119; CHAIN: A, B;	OXIDOREDUCTASE THERMOPHILIC, CYTOCHROMO P450, CRYSTAL STRUCTURE
1722	1io7	A	277	502	7.2e-36	-0.30	0.04		CYTOCHROME P450 CYP119; CHAIN: A, B;	OXIDOREDUCTASE THERMOPHILIC, CYTOCHROMO P450, CRYSTAL STRUCTURE
1722	1qmq	A	121	525	2.4e-35	0.55	1.00		CYTOCHROME P450; CHAIN: A;	OXIDOREDUCTASE CAMPHOR 5-MONOOXYGENASE OXIDOREDUCTASE(OXYGENASE) ,RU-SUBSTRATE,
1722	1qmq	A	88	533	2.4e-35			90.48	CYTOCHROME P450; CHAIN: A;	OXIDOREDUCTASE CAMPHOR 5-MONOOXYGENASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1725	1cdy		35	117	0.00036	0.28	0.19		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: NULL;	OXIDOREDUCTASE(OXYGENASE), RU-SUBSTRATE, T-CELL SURFACE GLYCOPROTEIN IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC, LIPOPROTEIN, T-CELL SURFACE GLYCOPROTEIN
1725	1cvs	D	35	149	0.00048	-0.04	0.04		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1725	1eaj	A	35	130	2.4e-06	0.15	0.30		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
1725	1evt	C	34	134	0.00096	0.16	0.72		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1725	1iil	G	35	117	0.0096	0.14	0.16		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1726	1cqk	A	11	105	1.1e-26			52.74	CH3 DOMAIN OF MAK33 ANTIBODY; CHAIN: A, B;	DOMAIN, B-TREFOIL IMMUNE SYSTEM CONSTANT DOMAIN, C1-SUBSET, IMMUNOGLOBULIN, IMMUNE SYSTEM
1726	1cqk	A	65	173	7e-29			52.57	CH3 DOMAIN OF MAK33 ANTIBODY; CHAIN: A, B;	IMMUNE SYSTEM CONSTANT DOMAIN, C1-SUBSET, IMMUNOGLOBULIN, IMMUNE SYSTEM
1726	1dn2	A	68	269	5.6e-51			53.86	IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
1726	1e4k	A	60	269	2.8e-50			55.13	LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
1726	1es0	B	1	167	1.4e-29			56.11	H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN; CHAIN: A; 65 KD GLUTAMIC ACID DECARBOXYLASE+H-2 CLASS II CHAIN: B;	IMMUNE SYSTEM HISTOCOMPATIBILITY ANTIGEN, CLASS II MHC I-A(G7)
1726	1f3j	B	1	173	9.8e-33			50.10	H-2 CLASS II HISTOCOMPATIBILITY ANTIGEN; CHAIN: A, D; MHC CLASS II NOD; CHAIN: B, E; LYSOZYME C; CHAIN: P, Q;	IMMUNE SYSTEM HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE COMPLEX
1726	1fc2	D	1	170	2.8e-50			54.74	IMMUNOGLOBULIN IMMUNOGLOBULIN FC	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
1726	1fne	A	1	169	2.8e-14			52.32	MHC CLASS II I-EK, ALPHA CHAIN; CHAIN: A, C; MHC CLASS II I-EK, BETA CHAIN; CHAIN: B, D;	IMMUNE SYSTEM HISTOCOMPATIBILITY ANTIGEN, MHC, PEPTIDE, IMMUNE SYSTEM
1726	1fvl	A	1	169	4.2e-17			53.07	MAJOR HISTOCOMPATIBILITY COMPLEX ALPHA CHAIN; CHAIN: A, D; MAJOR HISTOCOMPATIBILITY COMPLEX BETA CHAIN; CHAIN: B, E; MYELIN BASIC PROTEIN; CHAIN: C, F;	IMMUNE SYSTEM MHC CLASS II DR2A
1726	1hdm	B	7	175	5.6e-24			51.34	CLASS II HISTOCOMPATIBILITY ANTIGEN, M ALPHA CHAIN: A; CLASS II HISTOCOMPATIBILITY ANTIGEN, M BETA CHAIN: B;	IMMUNE SYSTEM RING6, HLA-DMA; RING7, HLA-DMB; HISTOCOMPATIBILITY PROTEIN, IMMUNE SYSTEM
1726	1i1c	A	1	169	2.8e-40			54.94	IG GAMMA-2A CHAIN C REGION; CHAIN: A, B;	IMMUNE SYSTEM IGG2A; IGG, FC
1726	1pfc		57	173	1.4e-27			54.04	IMMUNOGLOBULIN P/FC(PRIME) FRAGMENT OF AN IG*G1 1PFC 4	
1726	2iad	A	2	175	9.8e-14			51.43	MHC CLASS II I-AD; CHAIN: A, B;	MHC II MHC II, CLASS II MHC I-AD
1729	1de4	C	549	594	9.8e-05	-0.32	0.21		HEMOCHROMATOSIS	METAL TRANSPORT

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1729	1di2	A	157	260	2.8e-13	-0.45	0.19		PROTEIN; CHAIN: A, D, G; BETA-2-MICROGLOBULIN; CHAIN: B, E, H; TRANSFERRIN RECEPTOR; CHAIN: C, F, I;	INHIBITOR/RECEPTOR HFE; HFE, HEREDITARY HEMOCHROMATOSIS, MHC CLASS I, TRANSFERRIN 2 RECEPTOR
1729	1di2	A	181	266	1.2e-19	-0.19	0.62		CLASS I ALPHA-1,2-MANNOSIDASE; CHAIN: A;	HYDROLASE ALPHA-ALPHA HELIX BARREL
1729	1di2	A	194	374	5.6e-41	-0.21	0.10		CLASS I ALPHA-1,2-MANNOSIDASE; CHAIN: A;	HYDROLASE ALPHA-ALPHA HELIX BARREL
1729	1fo3	A	120	365	1.2e-54	0.06	1.00		ALPHA1,2-MANNOSIDASE; CHAIN: A;	HYDROLASE ALPHA-ALPHA7 BARREL
1729	1fo3	A	159	269	2.8e-19	-0.01	0.27		ALPHA1,2-MANNOSIDASE; CHAIN: A;	HYDROLASE ALPHA-ALPHA7 BARREL
1731	1f88	A	7	327	4.2e-96			122.22	RHODOPSIN; CHAIN: A, B	SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL
1731	1f88	A	8	345	4.2e-96	0.05	0.21		RHODOPSIN; CHAIN: A, B	PROTEIN, VISUAL PIGMENT SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL
1731	1f88	B	2	314	5.6e-90			104.29	RHODOPSIN; CHAIN: A, B	PROTEIN, VISUAL PIGMENT SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL
1731	1f88	B	8	312	5.6e-90	-0.13	0.03		RHODOPSIN; CHAIN: A, B	PROTEIN, VISUAL PIGMENT SIGNALING PROTEIN PHOTORECEPTOR, G PROTEIN-COUPLED RECEPTOR, MEMBRANE PROTEIN, 2 RETINAL
1732	1a4k	B	36	256	1.1e-75			84.51	ANTIBODY FAB; CHAIN: L, H, A, B;	PROTEIN, VISUAL PIGMENT IMMUNOGLOBULIN IMMUNOGLOBULIN, ANTIBODY, CATALYTIC ANTIBODY, DIELS ALDER, 2 GERMLINE
1732	1ae6	H	35	260	1.4e-89	0.10	0.81		ANTIBODY CTM01; CHAIN: L, H;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB FRAGMENT, HUMANISATION
1732	1afv	H	35	263	5.6e-88	-0.02	0.95		HUMAN IMMUNODEFICIENCY VIRUS TYPE 1 CAPSID CHAIN: A, B; ANTIBODY FAB25.3 FRAGMENT; CHAIN: H, K, L, M;	COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN) HIV-1 CA, HIV CA, HIV P24, P24; FAB, FAB LIGHT CHAIN, FAB HEAVY CHAIN COMPLEX (VIRAL CAPSID/IMMUNOGLOBULIN), HIV, CAPSID PROTEIN, 2 P24
1732	1ai1	H	36	244	1.1e-75			84.63	FAB59.1; CHAIN: L, H; AIB142; CHAIN: P;	COMPLEX (ANTIBODY/PEPTIDE) COMPLEX (ANTIBODY/PEPTIDE), ANTIBODY, CONSTRAINED HIV-1 V3 2 LOOP PEPTIDE, IMMUNOGLOBULIN
1732	1aif	A	154	287	9.8e-49	0.54	0.88		ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
1732	1aif	A	34	256	2.8e-34			86.97	ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A) FAB; CHAIN: A, B, L, H	IMMUNOGLOBULIN IMMUNOGLOBULIN, C REGION, V REGION
1732	1b2w	L	154	287	1.4e-49	0.13	0.68		ANTIBODY (LIGHT	IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN); CHAIN: L; ANTIBODY (HEAVY CHAIN); CHAIN: H;	IMMUNOGLOBULIN; IMMUNOGLOBULIN ANTIBODY ENGINEERING, HUMANIZED AND CHIMERIC ANTIBODY, FAB, 2 X-RAY STRUCTURE, THREE-DIMENSIONAL STRYCTURE, GAMMA- 3 INTERFERON, IMMUNE SYSTEM
1732	1b6d	A	154	287	1.3e-48	0.34	0.76		IMMUNOGLOBULIN; CHAIN: A, B;	IMMUNOGLOBULIN IMMUNOGLOBULIN, KAPPA LIGHT-CHAIN DIMER HEADER
1732	1bj1	J	154	287	2.8e-50	0.26	0.71		FAB FRAGMENT; CHAIN: L, H, J, K; VASCULAR ENDOTHELIAL GROWTH FACTOR; CHAIN: V, W;	COMPLEX (ANTIBODY/ANTIGEN) FAB-12; VEGF; COMPLEX (ANTIBODY/ANTIGEN), ANGIOGENIC FACTOR
1732	1c5d	B	36	248	1.4e-68			85.03	MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC CHAIN: L, A; MONOCLONAL ANTIBODY AGAINST THE MAIN IMMUNOGENIC CHAIN: H, B;	IMMUNE SYSTEM IMMUNOGLOBULIN
1732	1ce1	H	36	255	8.4e-74			89.67	CAMPATH-1H:LIGHT CHAIN; CHAIN: L; CAMPATH-1H:HEAVY CHAIN; CHAIN: H; PEPTIDE ANTIGEN; CHAIN: P;	ANTIBODY THERAPEUTIC, ANTIBODY, CD52
1732	1cf8	H	36	247	2.8e-77			87.27	CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CARBOCATION, 2 CYCLIZATION CASCADE
1732	1cif	L	154	287	9.8e-49	0.28	0.74		CATALYTIC ANTIBODY 19A4 (LIGHT CHAIN); CHAIN: L; CATALYTIC ANTIBODY 19A4 (HEAVY CHAIN); CHAIN: H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, TERPENOID SYNTHASE, CARBOCATION, 2 CYCLIZATION CASCADE
1732	1cic	B	35	227	1.4e-85	-0.06	0.77		IG HEAVY CHAIN V REGIONS; CHAIN: A; IG HEAVY CHAIN V REGIONS; CHAIN: B; IG HEAVY CHAIN V REGIONS; CHAIN: C; IG HEAVY CHAIN V REGIONS; CHAIN: D;	IMMUNOGLOBULIN IMMUNOGLOBULIN, FAB COMPLEX, IDIOTOPE, ANTI-IDIOTOPE
1732	1dee	A	154	287	2.8e-50	0.25	0.68		IGM RF 2A2; CHAIN: A, C, E; IGM RF 2A2; CHAIN: B, D, F; IMMUNOGLOBULIN G BINDING PROTEIN A; CHAIN: G, H;	IMMUNE SYSTEM FAB-IBP COMPLEX CRYSTAL STRUCTURE 2.7A RESOLUTION BINDING 2 OUTSIDE THE ANTIGEN COMBINING SITE SUPERANTIGEN FAB VH3 3 SPECIFICITY
1732	1dqd	H	36	246	5.6e-78			91.69	FAB HGR-2 F6; CHAIN: L; FAB HGR-2 F6; CHAIN: H;	IMMUNE SYSTEM GLUCAGON RECEPTOR, MONOCLONAL ANTIBODY, FAB, RECEPTOR 2 ANTAGONIST, TYPICAL IMMUNOGLOBULIN FOLD, LIGHT CHAIN, HEAVY 3 CHAIN, ANTIGEN BINDING SITE, COMPLEMENTARITY-DETERMINING 4 REGIONS
1732	1dqq	B	36	251	1.4e-72			85.70	ANTI-LYSOZYME ANTIBODY HYHEL-63 (LIGHT CHAIN); CHAIN:	IMMUNE SYSTEM ANTI-LYSOZYME ANTIBODY, HYHEL-63, HEN EGG WHITE LYSOZYME

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									A, C; ANTI-LYSOZYME ANTIBODY HYHEL-63 (HEAVY CHAIN); CHAIN: B, D;	
1732	1dzb	A	35	260	7e-96	0.44	0.99		SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
1732	1dzb	A	36	259	7e-96			95.55	SCFV FRAGMENT 1F9; CHAIN: A, B; TURKEY EGG-WHITE LYSOZYME C; CHAIN: X, Y;	COMPLEX (ANTIBODY ANTIGEN) 1,4-BETA-N-ACETYLMURAMIDASE C; SINGLE-DOMAIN ANTIBODY, TURKEY EGG-WHITE LYSOZYME, 2 ANTIBODY-PROTEIN COMPLEX, SINGLE-CHAIN FV FRAGMENT
1732	1e6o	H	36	263	4.2e-88	0.14	0.95		IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L; IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H;	IMMUNOGLOBULIN FAB, ANTIBODY, ANTIGEN, HIV-1, P24, CA
1732	1eap	B	36	221	2.8e-80	-0.14	0.24		CATALYTIC ANTIBODY 17E8 COMPLEXED WITH PHENYL [1-(1-N-SUCCINYLAMINO)PENTYL] 1EAP 3 PHOSPHONATE 1EAP 4	
1732	1egj	H	36	227	7e-83	-0.06	0.47		CYTOKINE RECEPTOR COMMON BETA CHAIN PRECURSOR; CHAIN: A; ANTIBODY (LIGHT CHAIN); CHAIN: L; ANTIBODY (HEAVY	IMMUNE SYSTEM CYTOKINE RECEPTOR COMPLEXED TO AN ANTIBODY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1732	1f3r	B	36	273	2.8e-84			99.76	CHAIN); CHAIN: H ACETYLCHOLINE RECEPTOR ALPHA; CHAIN: A; FV ANTIBODY FRAGMENT; CHAIN: B;	IMMUNE SYSTEM IG-FOLD, IMMUNO COMPLEX, ANTIBODY-ANTIGEN, BETA-TURN
1732	1f58	H	36	246	4.2e-79			86.22	IGG1 ANTIBODY 58.2 (LIGHT CHAIN); CHAIN: L; IGG1 ANTIBODY 58.2 (HEAVY CHAIN); CHAIN: H; EXTERIOR MEMBRANE GLYCOPROTEIN(GP120); CHAIN: P;	IMMUNE SYSTEM FAB 58.2; FAB 58.2; V3 LOOP; IMMUNOGLOBULIN, FAB, HIV-1, GP120, V3, IMMUNE SYSTEM
1732	1f8t	H	36	246	2.8e-79			86.44	ANTIBODY FAB FRAGMENT (LIGHT CHAIN); CHAIN: L; ANTIBODY FAB FRAGMENT (HEAVY CHAIN); CHAIN: H	IMMUNE SYSTEM MONOCLONAL ANTIBODY, ANTIGEN-BINDING FRAGMENT, INTERLEUKIN- 2 2, X-RAY ANALYSIS, CRYSTAL
1732	1fai	H	35	229	5.6e-84	-0.05	0.49		IMMUNOGLOBULIN FAB FRAGMENT FROM A MONOCLONAL ANTI-ARSONATE ANTIBODY, R19.9 1FAI 3 (IGG2B,KAPPA) 1FAI 4	
1732	1fbi	H	35	263	2.8e-88	0.08	0.72		COMPLEX (ANTIBODY/ANTIGEN) FAB FRAGMENT OF THE MONOCLONAL ANTIBODY F9.13.7 (IGG1) 1FBI 3 COMPLEXED WITH LYSOZYME (E.C.3.2.1.17) 1FBI 4	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1732	1fig	L	34	256	2.8e-35			85.48	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (KAPPA LIGHT CHAIN) FAB' FRAGMENT 1FIG 3	
1732	1fvd	A	154	287	2.8e-49	0.20	0.60		IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1732	1fvd	B	34	264	1.4e-80			89.40	IMMUNOGLOBULIN FAB FRAGMENT OF HUMANIZED ANTIBODY 4D5, VERSION 4 1FVD 3	
1732	1gpo	H	36	247	2.8e-73			86.78	ANTIBODY M41; CHAIN: L, H, M, 1;	IMMUNOGLOBULIN PROTEIN ENGINEERING, ANTIBODY DESIGN, IMMUNOGLOBULIN 2 STRUCTURE, ANTIGEN-BINDING SITE, CANONICAL CONFORMATION, 3 COMPLEMENTARITY-DETERMINING REGION
1732	1iai	H	35	227	9.8e-83	0.10	0.74		IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 1IAI 5 CHAIN: L, H; 1IAI 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); 1IAI 9 CHAIN: M, I 1IAI 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1732	1iai	H	36	253	9.8e-83			86.17	IDIOTYPIC FAB 730.1.4 (IGG1) OF VIRUS 1IAI 5 CHAIN: L, H; 1IAI 7 ANTI-IDIOTYPIC FAB 409.5.3 (IGG2A); 1IAI 9 CHAIN: M, I 1IAI 10	COMPLEX (IMMUNOGLOBULIN IGG1/IGG2A)
1732	1igj	B	37	245	7e-81			84.57	IMMUNOGLOBULIN FAB (IGG2A,KAPPA) FRAGMENT (26-10)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									COMPLEX WITH DIGOXIN 1IGJA 1 1IGJA 2	
1732	1igt	B	36	292	8.4e-93	0.05	0.36		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1732	1lmk	A	36	260	9.8e-91	0.49	1.00		IMMUNOGLOBULIN ANTI-PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C DIABODY 1LMK 3 SYNONYMS: L5MK16 DIABODY, SINGLE-CHAIN FV DIMER 1LMK 4	
1732	1lmk	A	37	260	9.8e-91			101.55	IMMUNOGLOBULIN ANTI-PHOSPHATIDYLINOSITOL SPECIFIC PHOSPHOLIPASE C DIABODY 1LMK 3 SYNONYMS: L5MK16 DIABODY, SINGLE-CHAIN FV DIMER 1LMK 4	
1732	1mam	H	36	229	9.8e-79	0.12	0.60		IMMUNOGLOBULIN ANTIGEN-BINDING FRAGMENT (FAB) (IGG2B, KAPPA) 1MAM 3	
1732	1mfa		36	260	7e-50			84.82	IMMUNOGLOBULIN FV FRAGMENT (MURINE SE155-4) COMPLEX WITH THE TRISACCHARIDE: 1MFA	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									3 ALPHA-D-GALACTOSE(1-2)[ALPHA-D-ABEQUOSE(1-3)]ALPHA-1MFA 4 D-MANNOSE (P1-OME) (PART OF THE CELL-SURFACE CARBOHYDRATE 1MFA 5 OF PATHOGENIC SALMONELLA) 1MFA 6	
1732	1mrd	H	36	229	1.4e-83	-0.02	0.78		IMMUNOGLOBULIN IGG JEL 103 FAB FRAGMENT COMPLEXED WITH 1MRD 3 INOSINE-5'-DIPHOSPHATE 1MRD 4	
1732	1ngp	H	35	263	2.8e-89	0.06	0.60		N1G9 (IGG1=LAMBDA=); CHAIN: L, H;	IMMUNOGLOBULIN
1732	1nqb	A	36	261	2.8e-98	0.51	0.99		SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN, IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
1732	1nqb	A	37	261	2.8e-98			95.40	SINGLE-CHAIN ANTIBODY FRAGMENT; CHAIN: A, C;	IMMUNOGLOBULIN VARIABLE HEAVY (VH) DOMAIN, VARIABLE LIGHT (VL) ANTIBODY FRAGMENT, MULTIVALENT ANTIBODY, DIABODY, DOMAIN 2 SWAPPING, IMMUNOGLOBULIN
1732	1osp	H	36	242	8.4e-72			96.00	FAB 184.1; CHAIN: L, H; OUTER SURFACE PROTEIN A; CHAIN: O;	COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN) OSPA; COMPLEX (IMMUNOGLOBULIN/LIPOPROTEIN), OUTER SURFACE 2 PROTEIN A COMPLEXED WITH FAB184.1,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BORRELIA BURGDORFERI 3 STRAIN B31
1732	1plg	H	35	227	7e-87	-0.18	0.71		IGG2A=KAPPA=; 1PLG 4 CHAIN: L, H; 1PLG 5	IMMUNOGLOBULIN
1732	1qkz	H	36	227	2.8e-82	0.11	0.42		ANTIBODY; CHAIN: H, L; PROTEIN G-PRIME; CHAIN: A; MAJOR OUTER MEMBRANE PROTEIN P1.16; CHAIN: P;	IMMUNE SYSTEM FAB, PORA, NEISSERIA MENINGITIDIS, PORIN
1732	1qok	A	35	260	2.8e-94	0.40	0.89		MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
1732	1qok	A	36	260	2.8e-94			95.49	MFE-23 RECOMBINANT ANTIBODY FRAGMENT; CHAIN: A;	IMMUNOGLOBULIN IMMUNOGLOBULIN, SINGLE-CHAIN FV, ANTI-CARCINOEMBRYONIC 2 ANTIGEN
1732	1sbs	L	154	287	7e-48	0.20	0.47		MONOCLONAL ANTIBODY 3A2; CHAIN: H, L;	MONOCLONAL ANTIBODY MONOCLONAL ANTIBODY, FAB-FRAGMENT, REPRODUCTION
1732	25c8	L	154	287	5.6e-50	0.42	0.69		IGG 5C8; CHAIN: L, H;	CATALYTIC ANTIBODY CATALYTIC ANTIBODY, FAB, RING CLOSURE REACTION
1732	2cgr	H	36	229	5.6e-81	-0.06	0.51		IMMUNOGLOBULIN IGG2B (KAPPA) FAB FRAGMENT COMPLEXED WITH ANTIGEN 2CGR 3 N-(P-CYANOPHENYL)-N'-(DIPHENYLEMETHYL) GUANIDINEACETIC ACID 2CGR 4	IMMUNOGLOBULIN FAB
1732	2fgw	L	154	287	5.6e-50	0.26	0.63			

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FRAGMENT OF A HUMANIZED VERSION OF THE ANTI-CD18 2FGW 3 ANTIBODY 'H52' (HUH52-OZ FAB) 2FGW 4	
1732	32c2	B	36	245	4.2e-77			85.02	IGG1 ANTIBODY 32C2; CHAIN: A; IGG1 ANTIBODY 32C2; CHAIN: B;	IMMUNE SYSTEM FAB, ANTIBODY, AROMATASE, P450
1732	3hfm	H	36	246	8.4e-74			92.13	COMPLEX(ANTIBODY-ANTIGEN) IG*G1 FAB FRAGMENT (HV/HEL$-10) AND LYSOZYME (E.C.3.2.1.17) 3HFM 4 COMPLEX 3HFM 5	
1734	1dt6	A	51	492	7e-74			67.96	CYTOCHROME P450 2C5; CHAIN: A;	OXIDOREDUCTASE PROGESTERONE 21-HYDROXYLASE, CYPIIC5 P450 1, MEMBRANE PROTEIN, PROGESTERONE 21-HYDROXYLASE, BENZO(A) 2 PYRENE HYDROXYLASE, ESTRADIOL 2-HYDROXYLASE, P450, CYP2C5
1739	1dg3	A	1	472	7e-91			73.28	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1739	1dg3	A	73	373	7e-91	-0.16	0.21		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GUANINE NUCLEOTIDE- BINDING PROTEIN 1; GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										DYNAMIN 2 RELATED, LARGE GTPASE FAMILY, SIGNALING PROTEIN
1739	1f5n	A	1	472	0			88.75	INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPPNP, GPPNHP.
1739	1f5n	A	65	373	0	0.15	0.74		INTERFERON-INDUCED GUANYLATE-BINDING PROTEIN 1; CHAIN: A;	SIGNALING PROTEIN GBP, GTP HYDROLYSIS, GDP, GMP, INTERFERON INDUCED, DYNAMIN 2 RELATED, LARGE GTPASE FAMILY. GMPPNP, GPPNHP.
1742	1byw	A	371	402	0.0024	-0.24	0.05		HUMAN ERG POTASSIUM CHANNEL; CHAIN: A;	MEMBRANE PROTEIN PAS DOMAIN, POTASSIUM CHANNEL DOMAIN, MEMBRANE PROTEIN
1742	1d06	A	363	463	1.1e-11	0.55	0.74		NITROGEN FIXATION REGULATORY PROTEIN FIXL; CHAIN: A;	SIGNALING PROTEIN OXYGEN SENSOR, HISTIDINE KINASE, PAS, HIGH-RESOLUTION, TWO- 2 COMPONENT SYSTEM
1742	1d06	A	469	540	4.8e-05	0.24	0.78		NITROGEN FIXATION REGULATORY PROTEIN FIXL; CHAIN: A;	SIGNALING PROTEIN OXYGEN SENSOR, HISTIDINE KINASE, PAS, HIGH-RESOLUTION, TWO- 2 COMPONENT SYSTEM
1742	1d06	A	573	618	0.0043	0.22	0.69		NITROGEN FIXATION REGULATORY PROTEIN FIXL; CHAIN: A;	SIGNALING PROTEIN OXYGEN SENSOR, HISTIDINE KINASE, PAS, HIGH-RESOLUTION, TWO- 2 COMPONENT SYSTEM
1742	1d06	A	574	616	8.4e-06	0.28	0.99		NITROGEN FIXATION REGULATORY PROTEIN FIXL; CHAIN: A;	SIGNALING PROTEIN OXYGEN SENSOR, HISTIDINE KINASE, PAS, HIGH-RESOLUTION, TWO- 2 COMPONENT SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1742	1dp6	A	359	465	8.4e-11	0.65	0.75		FIXL PROTEIN; CHAIN: A;	OXYGEN STORAGE/TRANSPORT FIXL, HEME, PAS DOMAIN, SIGNAL TRANSDUCTION, HISTIDINE 2 KINASE
1742	1dp6	A	360	462	1.2e-09	0.40	0.80		FIXL PROTEIN; CHAIN: A;	OXYGEN STORAGE/TRANSPORT FIXL, HEME, PAS DOMAIN, SIGNAL TRANSDUCTION, HISTIDINE 2 KINASE
1742	1dp6	A	469	542	7.2e-05	0.48	0.42		FIXL PROTEIN; CHAIN: A;	OXYGEN STORAGE/TRANSPORT FIXL, HEME, PAS DOMAIN, SIGNAL TRANSDUCTION, HISTIDINE 2 KINASE
1742	1dp6	A	574	616	0.00012	0.82	0.34		FIXL PROTEIN; CHAIN: A;	OXYGEN STORAGE/TRANSPORT FIXL, HEME, PAS DOMAIN, SIGNAL TRANSDUCTION, HISTIDINE 2 KINASE
1742	1g28	A	579	614	0.0006	0.34	0.46		PHY3 PROTEIN; CHAIN: A, B, C, D;	SIGNALING PROTEIN, ELECTRON TRANSPORT PHOTOTROPIN, LOV, PAS FOLD, PHOTORECEPTOR, FLAVOPROTEIN, 2 FMN-BINDING DOMAIN, ALPHA-BETA STRUCTURE
1745	1cfe		30	176	4.2e-14	0.78	1.00		PATHOGENESIS-RELATED PROTEIN P14A; CHAIN: NULL;	PATHOGENESIS-RELATED PROTEIN PATHOGENESIS-RELATED LEAF PROTEIN 6, ETHYLENE PATHOGENESIS-RELATED PROTEIN, PR-1 PROTEINS, 2 PLANT DEFENSE
1745	1qnx	A	1	170	4.2e-22	0.29	0.87		VES V 5; CHAIN: A;	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
1745	1qnx	A	28	185	1.2e-37	0.33	1.00		VES V 5; CHAIN: A;	ALLERGEN ANTIGEN 5; ANTIGEN 5, ALLERGEN, VESPID VENOM
1749	1ew3	A	27	75	1.4e-18	-0.58	0.96		ALLERGEN EQU C 1; CHAIN: A;	ALLERGEN LIPOCALIN, BETA BARREL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1749	1i06	A	42	75	2.4e-07	-0.37	0.94		MAJOR URINARY PROTEIN I; CHAIN: A;	TRANSPORT PROTEIN ALPHA-2U-GLOBULIN I; LIPOCALIN, BETA-BARREL, PHEROMONE
1749	2a2u	A	27	75	9.8e-16	-0.24	0.84		ALPHA-2U-GLOBULIN; CHAIN: A, B, C, D	LIPID BINDING PROTEIN A2U-GLOBULIN, LIPID BINDING PROTEIN
1753	1bih	A	148	511	5.6e-41	0.17	0.46		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1753	1bih	A	149	511	2.8e-51			101.99	HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1753	1bih	A	247	611	2.8e-40	0.30	0.42		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1753	1bih	A	59	416	2.8e-51	0.13	-0.07		HEMOLIN; CHAIN: A, B;	INSECT IMMUNITY INSECT IMMUNITY, LPS-BINDING, HOMOPHILIC ADHESION
1753	1cfb		511	685	1.3e-12	0.39	-0.08		NEURAL ADHESION MOLECULE DROSOPHILA NEUROGLIAN (CHYMOTRYPTIC FRAGMENT CONTAINING THE 1CFB 3 TWO AMINO PROXIMAL FIBRONECTIN TYPE III REPEATS 1CFB 4 (RESIDUES 610 - 814)) 1CFB 5	
1753	1cs6	A	142	513	1.4e-59			126.96	AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1753	1cs6	A	148	512	1.4e-54	0.20	0.11		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										ADHESION
1753	1cs6	A	247	612	4.2e-50	0.19	0.93		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1753	1cs6	A	57	416	1.4e-59	0.12	0.17		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1753	1cvs	C	159	325	2.8e-29	0.10	0.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1cvs	C	240	415	1.1e-34	0.32	-0.05		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1cvs	D	159	325	2.8e-30	0.01	0.06		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1cvs	D	240	415	5.6e-36	0.15	0.00		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1cvs	D	325	512	8.4e-37	0.01	-0.12		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1cvs	D	417	611	2.8e-32	0.03	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1cvs	D	58	235	4.2e-32	0.15	-0.11		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1753	1dgi	R	243	511	2.4e-21	-0.09	0.05		POLIOVIRUS RECEPTOR; CHAIN: R; VP1; CHAIN: 1; VP2; CHAIN: 2; VP3; CHAIN: 3; VP4; CHAIN: 4;	VIRUS/VIRAL PROTEIN, RECEPTOR CD155, PVR, HUMAN POLIOVIRUS, ELECTRON MICROSCOPY, 2 POLIOVIRUS-RECEPTOR COMPLEX, VIRUS/VIRAL PROTEIN, RECEPTOR
1753	1dn2	A	330	500	1.4e-25	-0.07	0.22		IMMUNOGLOBULIN LAMBDA HEAVY CHAIN; CHAIN: A, B; ENGINEERED PEPTIDE; CHAIN: E, F;	IMMUNE SYSTEM FC IGG PHAGE DISPLAY PEPTIDE
1753	1dx5	I	2	121	4.2e-17			55.65	THROMBIN LIGHT CHAIN; CHAIN: A, B, C, D; THROMBIN HEAVY	SERINE PROTEINASE COAGULATION FACTOR II; COAGULATION FACTOR II;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STRAT AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN; CHAIN: M, N, O, P; THROMBOMODULIN; CHAIN: I, J, K, L; THROMBIN INHIBITOR L-GLU-L-GLY-L-ARM; CHAIN: E, F, G, H;	FETOMODULIN, TM, CD141 ANTIGEN; EGR-CMK SERINE PROTEINASE, EGF-LIKE DOMAINS, ANTICOAGULANT COMPLEX, 2 ANTIFIBRINOLYTIC COMPLEX
1753	1e4k	A	330	500	1.1e-25	-0.04	0.01		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC RECEPTOR CHAIN: C; FC FRAGMENT OF HUMAN IGG1; CHAIN: A, B;	COMPLEX CD16; IGG1-FC COMPLEX, FC FRAGMENT, IGG, FC, RECEPTOR, CD16, GAMMA
1753	1eaj	A	33	145	0.0036	-0.03	0.03		COXSACKIE VIRUS AND ADENOVIRUS RECEPTOR; CHAIN: A, B;	VIRUS/VIRAL PROTEIN RECEPTOR COXSACKIEVIRUS B-ADENOVIRUS RECEPTOR, HCAR, VIRUS/VIRAL PROTEIN RECEPTOR, IMMUNOGLOBULIN V DOMAIN FOLD, 2 SYMMETRIC DIMER
1753	1emn		36	121	4.2e-20			60.14	FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1753	1epf	A	253	399	1.4e-21	0.29	0.36		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1753	1epf	A	335	495	2.8e-21	0.02	-0.12		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1753	1epf	A	424	595	1.1e-21	0.12	-0.02		NEURAL CELL ADHESION MOLECULE;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1753	1epf	A	54	235	5.6e-26	0.23	-0.01		CHAIN: A, B, C, D; NEURAL CELL ADHESION MOLECULE;	GLYCOPROTEIN CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1753	1ev2	E	243	415	1.3e-31	0.11	-0.18		CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	FIBROBLAST GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1ev2	E	429	611	9.8e-31	0.27	-0.03		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1ev2	G	243	419	2.8e-35	0.16	-0.08		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1ev2	G	429	615	1.3e-33	0.02	-0.09		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1evt	C	159	325	5.6e-30	-0.05	0.06		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1753	1evt	C	240	415	4.2e-35	0.16	-0.14		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1evt	C	325	512	1.4e-35	0.05	-0.18		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1evt	C	417	611	1.4e-31	0.02	-0.11		FIBROBLAST GROWTH FACTOR 1; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF1; FGFR1; IMMUNOGLOBULIN (IG) LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1753	1f2q	A	247	420	2.8e-18	0.45	0.63		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1753	1f2q	A	330	515	7e-18	0.15	-0.11		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN
1753	1f6a	A	149	331	4.8e-23	-0.11	0.13		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1753	1f6a	A	247	419	4.2e-17	0.48	0.70		HIGH AFFINITY	IMMUNE SYSTEM HIGH AFFINITY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1753	1f97	A	155	320	1.4e-25	0.47	0.87		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1753	1f97	A	254	410	8.4e-29	0.26	-0.05		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1753	1f97	A	421	606	1.4e-26	0.24	0.05		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1753	1f97	A	59	231	4.2e-27	0.09	0.60		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1753	1fc2	D	330	500	1.1e-25	0.06	0.59		IMMUNOGLOBULIN IMMUNOGLOBULIN FC AND FRAGMENT B OF PROTEIN A COMPLEX 1FC2 4	
1753	1fcg	A	149	327	1.2e-22	0.26	0.77		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1753	1fcg	A	239	401	8.4e-17	0.16	0.88		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1753	1fcg	A	329	512	2.8e-19	0.52	-0.17		FC RECEPTOR FC(GAMMA)RIIA; CHAIN: A;	IMMUNE SYSTEM, MEMBRANE PROTEIN CD32; FC RECEPTOR, IMMUNOGLOULIN, LEUKOCYTE, CD32
1753	1fnl	A	239	401	2.4e-16	0.34	1.00		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1753	1hj7	A	39	121	1.4e-19			51.87	LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1753	1hzh	H	259	614	5.6e-17	0.01	-0.09		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
1753	1hzh	H	62	404	1.4e-22	0.24	0.60		IMMUNOGLOBULIN HEAVY CHAIN; CHAIN: H, K; IMMUNOGLOBULIN LIGHT CHAIN; CHAIN: L, M;	IMMUNE SYSTEM IGG; IMMUNOGLOBULIN, ANTIBODY, B12
1753	1ilc	A	332	506	1.4e-20	0.25	0.09		IG GAMMA-2A CHAIN C REGION; CHAIN: A, B;	IMMUNE SYSTEM IGG2A; IGG, FC
1753	1ilr	A	348	611	8.4e-15	0.05	-0.08		INTERLEUKIN-6 RECEPTOR BETA CHAIN; CHAIN: A; VIRAL IL-6; CHAIN: B;	CYTOKINE GP130; FUNCTIONAL INTERLEUKIN-6 HOMOLOG; CYTOKINE/RECEPTOR COMPLEX, GP130, VIRAL IL-6, CRYSTAL 2 STRUCTURE
1753	1ie5	A	323	415	1.4e-15	0.10	-0.11		NEURAL CELL ADHESION MOLECULE;	CELL ADHESION N-CAM; INTERMEDIATE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1753	1igt	B	159	499	1.1e-25	-0.12	0.24		CHAIN: A; IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN FOLD IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1753	1igt	B	66	410	1.3e-22	0.15	-0.12		IGG2A INTACT ANTIBODY - MAB231; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN V REGION C REGION, IMMUNOGLOBULIN
1753	1igy	B	64	410	5.6e-23	-0.22	0.19		IGG1 INTACT ANTIBODY MAB61.1.3; CHAIN: A, B, C, D	IMMUNOGLOBULIN INTACT IMMUNOGLOBULIN, V REGION, C REGION, HINGE REGION
1753	1iil	G	159	329	5.6e-27	0.24	0.13		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1753	1iil	G	243	419	1.4e-34	0.26	0.04		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1753	1iil	G	429	615	9.8e-36	0.23	-0.08		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1753	1itb	B	169	413	1.3e-16	0.10	-0.11		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RECEPTOR; CHAIN: B;	TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1753	1itb	B	352	609	2.8e-19	0.24	-0.15		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1753	1itb	B	39	326	3.6e-21	-0.03	0.12		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1753	1mco	H	123	511	4.2e-37			100.32	IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1753	1mco	H	54	404	1.4e-26	-0.07	0.74		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1753	1nct		248	326	1.3e-16	0.05	0.13		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1753	1nct		519	612	2.8e-10	0.07	-0.19		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1753	1neu		43	130	0.0072	-0.02	0.11		MYELIN P0 PROTEIN; CHAIN: NULL;	STRUCTURAL PROTEIN MYELIN, STRUCTURAL PROTEIN, GLYCOPROTEIN, TRANSMEMBRANE, PHOSPHORYLATION, IMMUNOGLOBULIN FOLD, SIGNAL, MYELIN 2 MEMBRANE ADHESION MOLECULE
1753	1qg3	A	487	615	1.2e-09	0.21	-0.15		INTEGRIN BETA-4 SUBUNIT; CHAIN: A, B;	STRUCTURAL PROTEIN INTEGRIN, HEMIDESMOSOME, FIBRONECTIN, CARCINOMA, STRUCTURAL 2 PROTEIN
1753	1qr4	A	487	610	1.2e-10	0.37	-0.08		TENASCIN; CHAIN: A, B;	STRUCTURAL PROTEIN TENASCIN, FIBRONECTIN TYPE-III, HEPARIN, EXTRACELLULAR 2 MATRIX, ADHESION, FUSION PROTEIN, STRUCTURAL PROTEIN
1753	1tnm		248	326	1.3e-16	0.40	0.11		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1753	1tnm		519	612	2.8e-10	0.23	-0.17		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1753	1wio	A	161	508	2.4e-22	0.04	-0.15		1TNM 4 1TNM 58 T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1753	1wio	A	44	402	4.8e-24	0.19	-0.17		T-CELL SURFACE GLYCOPROTEIN CD4; CHAIN: A, B;	GLYCOPROTEIN CD4; IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, T-CELL, 2 MHC LIPOPROTEIN, POLYMORPHISM
1753	2dli	A	149	314	4.8e-21	-0.20	0.39		MHC CLASS I NK CELL RECEPTOR PRECURSOR; CHAIN: A;	IMMUNE SYSTEM P58 NATURAL KILLER CELL RECEPTOR; KIR, NATURAL KILLER RECEPTOR, INHIBITORY RECEPTOR, 2 IMMUNOGLOBULIN
1753	2fcb	A	239	401	9.6e-16	0.21	0.76		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1753	2fcb	A	329	514	5.6e-19	0.21	-0.15		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1753	2ncm		54	143	5.6e-09	0.09	-0.12		NEURAL CELL ADHESION MOLECULE; CHAIN: NULL;	CELL ADHESION NCAM DOMAIN 1; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, SIGNAL
1753	3ncm	A	55	141	2.8e-08	-0.00	-0.19		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1753	8fab	A	334	507	2.8e-16	-0.00	-0.09		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1753	8fab	A	421	599	1.1e-15	0.06	-0.18		IMMUNOGLOBULIN FAB FRAGMENT FROM HUMAN IMMUNOGLOBULIN IGG1 (LAMBDA, HIL) 8FAB 3	
1757	1hd7	A	367	630	1.2e-14	-0.08	0.06		DNA-(APURINIC OR APYRIMIDINIC SITE) LYASE; CHAIN: A;	DNA REPAIR AP ENDONUCLEASE 1, HAP1, REF1, APE1; DNA REPAIR, ENDONUCLEASE, APE1, HAP1, REF-1
1757	1i9z	A	1	279	5.6e-86			109.20	PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE; CHAIN: A;	HYDROLASE SYNAPTOJANIN; SPSYNAPTOJANIN, IPP5C, IP3, IP2,
1757	1i9z	A	345	702	1.3e-86			143.57	PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE; CHAIN: A;	HYDROLASE SYNAPTOJANIN; SPSYNAPTOJANIN, IPP5C, IP3, IP2,
1757	1i9z	A	359	627	1.3e-86	0.62	1.00		PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE; CHAIN: A;	HYDROLASE SYNAPTOJANIN; SPSYNAPTOJANIN, IPP5C, IP3, IP2,
1757	1i9z	A	363	621	4.8e-71	0.54	1.00		PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE; CHAIN:	HYDROLASE SYNAPTOJANIN; SPSYNAPTOJANIN, IPP5C, IP3, IP2,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1757	1i9z	A	750	789	0.00098	-0.33	0.39		A; PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE; CHAIN: A;	HYDROLASE SYNAPTOJANIN; SPSYNAPTOJANIN, IPP5C, IP3, IP2,
1757	1i9z	A	753	791	1.2e-09	-0.36	0.47		PHOSPHATIDYLINOSITOL PHOSPHATE PHOSPHATASE; CHAIN: A;	HYDROLASE SYNAPTOJANIN; SPSYNAPTOJANIN, IPP5C, IP3, IP2,
1758	1qdv	A	107	214	1.4e-28	0.18	0.12		KV1.2 VOLTAGE-GATED POTASSIUM CHANNEL; CHAIN: A, B, C, D;	SIGNALING PROTEIN VOLTAGE-GATED POTASSIUM CHANNEL, TETRAMERIZATION DOMAIN, 2 INTRACELLULAR GATE, TETRAMER
1759	1esj	A	260	524	1.1e-16	0.45	0.23		HYDROXYETHYLTHIAZOLE KINASE; CHAIN: A, B, C;	TRANSFERASE THZ KINASE; TRIMER, ALPHA-BETA PROTEIN
1763	1a4y	A	60	364	2.4e-38	0.32	0.93		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1763	1a9n	A	152	306	1.2e-15	0.09	0.03		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	A	176	341	1.2e-14	0.42	-0.03		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	A	210	361	4.8e-13	0.49	0.23		U2 RNA HAIRPIN IV;	COMPLEX (NUCLEAR

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'';	PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,
1763	1a9n	A	255	361	1.4e-06	0.20	0.60		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	SNRNP,RIBONUCLEOPROTEIN COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	A	63	169	5.6e-06	0.38	0.30		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	A	67	216	2.4e-22	0.47	0.33		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	A	91	234	3.6e-21	0.75	0.96		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	C	210	374	6e-13	0.26	-0.07		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	C	255	361	1.4e-06	-0.04	0.72		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1a9n	C	67	237	1.2e-23	0.44	0.51		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1763	1cs6	A	412	518	2.4e-16	0.27	0.11		AXONIN-1; CHAIN: A;	CELL ADHESION NEURAL CELL ADHESION
1763	1cvs	C	417	519	2.4e-14	0.46	0.17		FIBROBLAST GROWTH	GROWTH FACTOR/GROWTH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1763	1cvs	D	417	518	7.2e-15	0.38	0.10		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1763	1cvs	D	420	502	6e-16	0.52	0.65		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B; FIBROBLAST GROWTH FACTOR RECEPTOR 1; CHAIN: C, D;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF, FGFR, IMMUNOGLOBULIN-LIKE, SIGNAL TRANSDUCTION, 2 DIMERIZATION, GROWTH FACTOR/GROWTH FACTOR RECEPTOR
1763	1d0b	A	128	331	1.1e-21	0.13	0.37		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1763	1d0b	A	248	402	1.4e-20	0.16	0.98		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1763	1d0b	A	42	195	4.2e-19	0.45	0.90		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1763	1d0b	A	59	283	1.4e-18	-0.15	0.21		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1763	1d0b	A	61	236	1.1e-19	0.68	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										CELL ADHESION
1763	1d0b	A	63	211	2.4e-20	0.35	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1763	1d0b	A	80	309	2.4e-20	0.46	0.90		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1763	1dce	A	135	288	8.4e-06	-0.11	0.06		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1763	1dce	A	231	353	5.6e-13	0.24	0.78		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1763	1dce	A	255	360	7e-12	0.08	1.00		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1763	1dce	A	42	168	1.4e-07	0.09	-0.03		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1763	1ds9	A	216	363	1.1e-12	-0.01	0.10		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1763	1ds9	A	240	363	5.6e-15	-0.28	0.12		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1763	1epf	A	420	518	7.2e-14	0.51	0.39		NEURAL CELL ADHESION MOLECULE; CHAIN: A, B, C, D;	CELL ADHESION NCAM; NCAM, IMMUNOGLOBULIN FOLD, GLYCOPROTEIN
1763	1ev2	E	417	518	4.8e-15	0.38	0.39		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1763	1ev2	G	420	507	1.2e-15	0.17	0.15		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD
1763	1f2q	A	411	518	2.4e-13	0.36	0.31		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A;	IMMUNE SYSTEM FC-EPSILON RI-ALPHA; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1763	1f6a	A	411	518	2.4e-14	0.23	0.22		HIGH AFFINITY IMMUNOGLOBULIN EPSILON RECEPTOR CHAIN: A; IG EPSILON CHAIN C REGION; CHAIN: B, D;	IMMUNE SYSTEM HIGH AFFINITY IGE-FC RECEPTOR, FC(EPSILON) IGE-FC; IMMUNOGLOBULIN FOLD, GLYCOPROTEIN, RECEPTOR, IGE-BINDING 2 PROTEIN, IGE ANTIBODY, IGE-FC
1763	1f97	A	411	518	8.4e-14	0.27	0.35		JUNCTION ADHESION MOLECULE; CHAIN: A;	CELL ADHESION IMMUNOGLOBULIN SUPERFAMILY, BETA-SANDWICH FOLD
1763	1fml	A	411	518	4.8e-14	0.42	0.01		LOW AFFINITY IMMUNOGLOBULIN GAMMA FC REGION CHAIN: A;	IMMUNE SYSTEM RECEPTOR BETA SANDWICH, IMMUNOGLOBULIN-LIKE, RECEPTOR
1763	1fo1	A	250	313	5.6e-07	-0.48	0.24		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1763	1fo1	A	78	138	7.2e-07	-0.27	0.33		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1763	1fo1	B	232	288	1.4e-05	0.01	0.03		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1763	1fo1	B	250	313	5.6e-07	-0.27	0.22		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1763	1fo1	B	65	113	3.6e-06	-0.30	0.25		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1763	1fqv	A	231	450	1.3e-08	0.16	-0.05		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1763	1fqv	A	255	526	7e-09	-0.00	-0.20		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1763	1fqv	A	30	283	7.2e-18	0.41	-0.12		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1763	1fqv	A	71	373	2.4e-17	0.04	-0.07		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1763	1ft8	A	250	313	5.6e-07	-0.25	0.04		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RIBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
1763	1iam		420	518	8.4e-16	0.10	0.04		INTERCELLULAR ADHESION MOLECULE-1; CHAIN: NULL;	RHINOVIRUS RECEPTOR ICAM-1, CD54; RHINOVIRUS RECEPTOR, CELL ADHESION, INTEGRIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										LIGAND, 2 GLYCOPROTEIN, LFA-1 LIGAND, IMMUNOGLOBULIN FOLD, 3 TRANSMEMBRANE
1763	1iil	G	420	518	4.8e-15	0.30	0.27		HEPARIN-BINDING GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2, HBGF-2, BASIC FIBROBLAST GROWTH FACTOR, FGFR2, KERATINOCYTE GROWTH FACTOR RECEPTOR; IMMUNOGLOBULIN LIKE DOMAIN, B-TREFOIL
1763	1iib	B	420	519	2.4e-13	0.17	-0.14		INTERLEUKIN-1 BETA; CHAIN: A; TYPE 1 INTERLEUKIN-1 RECEPTOR; CHAIN: B;	COMPLEX (IMMUNOGLOBULIN/RECEPTOR) IMMUNOGLOBULIN FOLD, TRANSMEMBRANE, GLYCOPROTEIN, RECEPTOR, 2 SIGNAL, COMPLEX (IMMUNOGLOBULIN/RECEPTOR)
1763	1nct		409	501	1.1e-16	0.58	0.82		TITIN; CHAIN: NULL;	MUSCLE PROTEIN CONNECTIN, NEXTM5; CELL ADHESION, GLYCOPROTEIN, TRANSMEMBRANE, REPEAT, BRAIN, 2 IMMUNOGLOBULIN FOLD, ALTERNATIVE SPLICING, SIGNAL, 3 MUSCLE PROTEIN
1763	1tnm		1	79	5.6e-18			53.79	MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE) 1TNM 4 1TNM 58	
1763	1tnm		420	501	3.6e-16	0.55	1.00		MUSCLE PROTEIN TITIN MODULE M5 (CONNECTIN) 1TNM 3 (NMR, MINIMIZED AVERAGE STRUCTURE)	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1763	1yrg	A	173	379	1.2e-13	0.26	0.25		1TNM 4 1TNM 58	
									GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1763	1yrg	A	65	289	9.6e-21	0.17	-0.02		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1763	1yrg	A	81	360	6e-24	0.42	0.31		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1763	2bnh		1	446	7.2e-36			83.20	RIBONUCLEASE INHIBITOR, CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1763	2bnh		60	405	4.2e-13	0.15	0.23		RIBONUCLEASE INHIBITOR; CHAIN:	ACETYLATION RNASE INHIBITOR,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									NULL;	RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1763	2bnh		65	364	7.2e-36	0.33	0.75		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1763	2fcb	A	411	518	2.4e-13	0.19	-0.01		FC GAMMA RIIB; CHAIN: A;	IMMUNE SYSTEM CD32; RECEPTOR, FC, CD32, IMMUNE SYSTEM
1763	3ncm	A	420	502	1.2e-15	0.30	0.92		NEURAL CELL ADHESION MOLECULE, LARGE ISOFORM; CHAIN: A;	CELL ADHESION PROTEIN NCAM MODULE 2; CELL ADHESION, GLYCOPROTEIN, HEPARIN-BINDING, GPI-ANCHOR, 2 NEURAL ADHESION MOLECULE, IMMUNOGLOBULIN FOLD, HOMOPHILIC 3 BINDING, CELL ADHESION PROTEIN
1764	1atl	A	152	359	1.3e-28	0.81	1.00		ATROLYSIN C; 1ATL 4 CHAIN: A, B, C, D; 1ATL 5	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM D; 1ATL 6
1764	1atl	A	156	359	1.2e-37	0.83	1.00		ATROLYSIN C; 1ATL 4 CHAIN: A, B, C, D; 1ATL 5	METALLOENDOPEPTIDASE HEMORRHAGIC TOXIN C, FORM D; 1ATL 6
1764	1bkc	A	156	357	3.6e-40	0.20	0.77		TUMOR NECROSIS FACTOR-ALPHA-CONVERTING ENZYME; CHAIN: A, C, E, I;	ZN-ENDOPEPTIDASE TACE; ZN-ENDOPEPTIDASE, HYDROLASE, TNF-ALPHA
1764	1bud	A	154	357	7e-27	0.68	1.00		ACUTOLYSIN A; CHAIN: A;	TOXIN HEMORRHAGIN I, 1AAH-I; METALLOPROTEINASE, SNAKE VENOM, MMP, TOXIN
1764	1dva	L	519	596	1.4e-12	0.10	-0.18		DES-GLA FACTOR VIIA (HEAVY CHAIN); CHAIN:	HYDROLASE/HYDROLASE INHIBITOR PROTEIN-PEPTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									H, I; DES-GLA FACTOR VIIA (LIGHT CHAIN); CHAIN: L, M; (DPN)-PHE-ARG; CHAIN: C, D; PEPTIDE E-76; CHAIN: X, Y;	COMPLEX
1764	1emn		126	194	7e-14	0.03	-0.20		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1764	1emn		327	394	1.4e-11	0.12	-0.20		FIBRILLIN; CHAIN: NULL;	MATRIX PROTEIN EXTRACELLULAR MATRIX, CALCIUM-BINDING, GLYCOPROTEIN, 2 REPEAT, SIGNAL, MULTIGENE FAMILY, DISEASE MUTATION, 3 EGF-LIKE DOMAIN, HUMAN FIBRILLIN-1 FRAGMENT, MATRIX PROTEIN
1764	1hj7	A	358	438	4.2e-11	0.12	-0.20		LDL RECEPTOR; CHAIN: A;	CELL-SURFACE RECEPTOR CELL-SURFACE RECEPTOR, CALCIUM-BINDING, EGF-LIKE DOMAIN, 2 MODULE, APO-E, APO-B, LDL, VLDL
1764	1iag		152	359	2.8e-28	0.80	1.00		METALLOPROTEASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) 1IAG 3	
1764	1iag		156	359	1.2e-37	0.84	1.00		METALLOPROTEASE ADAMALYSIN II (PROTEINASE II) (E.C.3.4.24.46) 1IAG 3	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1764	1qua	A	152	357	5.6e-28	0.87	1.00		ACUTOLYSIN-C; CHAIN: A;	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRODON ACUTUS
1764	1qua	A	156	357	9.6e-32	0.77	1.00		ACUTOLYSIN-C; CHAIN: A;	TOXIN HEMORRHAGIN III METALLOPROTEASE, HEMORRHAGIC TOXIN, SNAKE VENOM PROTEINASE, 2 CRYSTAL STRUCTURE, AGKISTRODON ACUTUS
1764	9wga	A	400	568	8.4e-15	0.00	-0.19		LECTIN (AGGLUTININ) WHEAT GERM AGGLUTININ (ISOLECTIN 2) 9WGA 3	
1768	1ewk	A	40	295	7e-42	-0.20	0.10		METABOTROPIC GLUTAMATE RECEPTOR SUBTYPE 1; CHAIN: A, B;	SIGNALING PROTEIN MGLUR1; SIGNAL TRANSDUCTION, NEUROTRANSMITTER, CNS, NEURON
1768	1ewk	A	42	223	9.6e-20	0.39	1.00		METABOTROPIC GLUTAMATE RECEPTOR SUBTYPE 1; CHAIN: A, B;	SIGNALING PROTEIN MGLUR1; SIGNAL TRANSDUCTION, NEUROTRANSMITTER, CNS, NEURON
1768	2lbp		48	174	9.6e-08	-0.06	0.06		PERIPLASMIC BINDING PROTEIN LEUCINE-BINDING PROTEIN (/LBP$) 2LBP 4	
1768	2liv		48	142	0.00084	0.08	0.09		PERIPLASMIC BINDING PROTEIN LEUCINE(SLASH)*ISOLEUCINE(SLASH)*VALINE-BINDING PROTEIN 2LIV 4 (/LIVBP$) 2LIV 5	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1768	2liv		48	221	3.6e-12	-0.06	0.21		PERIPLASMIC BINDING PROTEIN LEUCINE(SLASH)*ISOLEUCINE(SLASH)*VALINE-BINDING PROTEIN 2LIV 4 (/LIVBP$) 2LIV 5	
1769	1a25	A	2	109	5.6e-33			55.91	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1769	1a25	A	366	498	5.6e-30			77.89	PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1769	1a25	A	369	495	5.6e-30	0.12	0.58		PROTEIN KINASE C (BETA); CHAIN: A, B;	CALCIUM-BINDING PROTEIN CALB; CALCIUM++/PHOSPHOLIPID BINDING PROTEIN, 2 CALCIUM-BINDING PROTEIN
1769	1byn	A	1	109	1.4e-36			80.43	SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
1769	1byn	A	1	109	7e-31			59.50	SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
1769	1byn	A	231	356	1.4e-33	0.55	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE,
										ENDOCYTOSIS/EXOCYTOSIS
1769	1byn	A	232	360	1.4e-33			95.19	SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1769	1byn	A	365	490	5.6e-23	0.21	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1769	1byn	A	367	493	9.6e-29	0.39	1.00		SYNAPTOTAGMIN I; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS SYNAPTOTAGMIN, C2-DOMAIN, EXOCYTOSIS, NEUROTRANSMITTER 2 RELEASE, ENDOCYTOSIS/EXOCYTOSIS
1769	1djx	A	223	377	2.4e-21	0.33	0.13		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3
1769	1djx	B	228	377	3.6e-22	0.22	0.55		PHOSPHOINOSITIDE-SPECIFIC PHOSPHOLIPASE C, CHAIN: A, B;	PHOSPHOINOSITIDE-SPECIFIC LIPID DEGRADATION PLC-D1; PHOSPHORIC DIESTER HYDROLASE, HYDROLASE, LIPID DEGRADATION, 2 TRANSDUCER, CALCIUM-BINDING, PHOSPHOLIPASE C, 3

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										PHOSPHOINOSTITDE-SPECIFIC
1769	1dqv	A	230	505	9.8e-65			235.90	SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1769	1dqv	A	233	504	9.8e-65	0.24	1.00		SYNAPTOTAGMIN III; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS BETA SANDWICH, CALCIUM ION, C2 DOMAIN
1769	1dsy	A	2	109	1.1e-33			57.02	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
1769	1dsy	A	366	504	4.2e-30			82.11	PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
1769	1dsy	A	369	495	4.2e-30	0.15	0.65		PROTEIN KINASE C, ALPHA TYPE; CHAIN: A;	TRANSFERASE CALCIUM++, PHOSPHOLIPID BINDING PROTEIN, CALCIUM-BINDING 2 PROTEIN, PHOSPHATIDYLSERINE, PROTEIN KINASE C
1769	1rlw		380	472	6e-20	0.07	-0.09		PHOSPHOLIPASE A2; CHAIN: NULL;	HYDROLASE CALB DOMAIN; HYDROLASE, C2 DOMAIN, CALB DOMAIN
1769	1rsy		1	109	1.4e-36			84.72	CALCIUM/PHOSPHOLIPID BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1769	1rsy		1	109	7e-31			61.17	CALCIUM/PHOSPHOLIPI	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									D BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1769	1rsy		223	359	1.4e-33			103.60	CALCIUM/PHOSPHOLIPI D BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1769	1rsy		231	356	1.4e-33	0.47	1.00		CALCIUM/PHOSPHOLIPI D BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1769	1rsy		363	490	2.8e-23	0.34	0.95		CALCIUM/PHOSPHOLIPI D BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1769	1rsy		367	491	4.8e-28	0.50	1.00		CALCIUM/PHOSPHOLIPI D BINDING PROTEIN SYNAPTOTAGMIN I (FIRST C2 DOMAIN) (CALB) 1RSY 3	
1769	3rpb	A	367	502	2.8e-31	0.45	1.00		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1769	3rpb	A	367	504	1.2e-38	0.42	0.92		RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN, RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1769	3rpb	A	367	505	1.2e-38			92.99	RABPHILIN 3-A; CHAIN: A;	ENDOCYTOSIS/EXOCYTOSIS C2-DOMAINS, C2B-DOMAIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										RABPHILIN, ENDOCYTOSIS/EXOCYTOSIS
1771	1edh	A	142	344	1.4e-49	0.09	0.95		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	23	127	1.3e-14	-0.15	0.25		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	251	452	1.2e-35	0.22	0.98		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	251	452	4.2e-29	-0.01	0.81		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	349	557	4.8e-46	0.27	1.00		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	35	236	1.2e-21	-0.22	0.04		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	360	539	1.4e-30	0.09	0.92		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	467	693	3.6e-27	0.12	0.47		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	494	697	7e-26	0.03	0.47		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1edh	A	66	236	1.4e-38	-0.34	0.39		E-CADHERIN; CHAIN: A, B;	CELL ADHESION PROTEIN EPITHELIAL CADHERIN DOMAINS 1 AND 2, ECAD12; CADHERIN, CELL ADHESION PROTEIN, CALCIUM BINDING PROTEIN
1771	1ncg		142	235	9.8e-17	0.17	-0.08		N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN CADHERIN 1NCG 13
1771	1ncg		251	343	8.4e-07	0.25	0.23		N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN CADHERIN 1NCG 13
1771	1ncg		255	343	4.8e-13	-0.18	0.01		N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN CADHERIN 1NCG 13
1771	1ncg		356	450	3.6e-06	0.05	0.51		N-CADHERIN; 1NCG 3	CELL ADHESION PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1771	1ncg		360	450	7e-05	0.00	0.06		N-CADHERIN; 1NCG 3	CADHERIN 1NCG 13
										CELL ADHESION PROTEIN
1771	1ncg		467	556	3.6e-10	0.34	0.13		N-CADHERIN; 1NCG 3	CADHERIN 1NCG 13
										CELL ADHESION PROTEIN
1771	1ncg		491	542	2.8e-06	-0.05	0.63		N-CADHERIN; 1NCG 3	CADHERIN 1NCG 13
										CELL ADHESION PROTEIN
1771	1ncg		631	695	0.0017	0.06	0.10		N-CADHERIN; 1NCG 3	CADHERIN 1NCG 13
										CELL ADHESION PROTEIN
1771	1nci	B	142	236	2.8e-16	0.14	0.09		N-CADHERIN; 1NCI 3	CADHERIN 1NCI 13
										CELL ADHESION PROTEIN
1771	1nci	B	277	344	7e-07	0.09	0.13		N-CADHERIN; 1NCI 3	CADHERIN 1NCI 13
										CELL ADHESION PROTEIN
1771	1nci	B	295	344	9.6e-09	-0.28	0.66		N-CADHERIN; 1NCI 3	CADHERIN 1NCI 13
										CELL ADHESION PROTEIN
1771	1nci	B	398	452	2.4e-07	-0.47	0.53		N-CADHERIN; 1NCI 3	CADHERIN 1NCI 13
										CELL ADHESION PROTEIN
1771	1nci	B	495	542	5.6e-06	0.05	0.17		N-CADHERIN; 1NCI 3	CADHERIN 1NCI 13
										CELL ADHESION PROTEIN
1771	1ncj	A	142	344	1.4e-52	0.17	0.83		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN
										CELL ADHESION PROTEIN
1771	1ncj	A	23	127	1.1e-15	-0.22	0.41		N-CADHERIN; CHAIN: A;	ADHESION PROTEIN CELL
										ADHESION PROTEIN
1771	1ncj	A	251	452	5.6e-31	0.04	0.99		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
										ADHESION PROTEIN
1771	1ncj	A	356	560	2.4e-37	-0.02	0.24		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
										ADHESION PROTEIN
1771	1ncj	A	360	543	8.4e-31	0.17	0.96		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
										ADHESION PROTEIN
1771	1ncj	A	488	697	2.8e-27	0.19	0.25		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
										ADHESION PROTEIN
1771	1ncj	A	605	716	4.2e-10	-0.22	0.05		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL
										ADHESION PROTEIN
1771	1ncj	A	66	236	8.4e-39	-0.45	0.36		N-CADHERIN; CHAIN: A;	CELL ADHESION PROTEIN CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1771	1suh		251	348	2.8e-09	0.15	0.51		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION PROTEIN CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING,
1771	1suh		253	348	2.4e-23	0.03	0.24		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1771	1suh		356	456	1.2e-15	0.06	0.17		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1771	1suh		360	456	8.4e-08	0.02	0.37		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1771	1suh		461	561	6e-24	0.39	0.46		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1771	1suh		494	561	5.6e-07	0.06	0.68		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1771	1suh		613	693	1.2e-09	0.28	-0.14		EPITHELIAL CADHERIN; CHAIN: NULL;	CELL ADHESION UVOMORULIN; CADHERIN, CALCIUM BINDING, CELL ADHESION
1778	1sfc	A	110	175	8.4e-25	-0.70	0.03		SYNAPTOBREVIN 2; CHAIN: A, E, I; SYNTAXIN 1A; CHAIN: B, F, J; SNAP-25B; CHAIN: C, G, K; SNAP-25B; CHAIN: D, H, L;	TRANSPORT PROTEIN VAMP 2; MEMBRANE FUSION PROTEIN COMPLEX, TRANSPORT PROTEIN
1780	1a17		76	242	5.6e-33			82.28	SERINE/THREONINE PROTEIN PHOSPHATASE 5; CHAIN: NULL;	HYDROLASE TETRATRICOPEPTIDE, TRP; HYDROLASE, PHOSPHATASE, PROTEIN-PROTEIN INTERACTIONS, TPR, 2 SUPER-HELIX, X-RAY STRUCTURE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1780	1aln	A	11	174	4.2e-74			125.43	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1780	1aln	A	25	274	0	0.68	1.00		B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1780	1aln	A	25	274	0			324.34	B*3501; CHAIN: A, B; PEPTIDE VPLRPMTY; CHAIN: C;	COMPLEX (ANTIGEN/PEPTIDE) B35; MAJOR HISTOCOMPATIBILITY ANTIGEN, MHC, HLA, HLA-B3501, HIV, 2 NEF, COMPLEX (ANTIGEN/PEPTIDE)
1780	1agd	A	11	174	2.8e-75			121.80	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1780	1agd	A	25	274	0	0.50	1.00		B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE); CHAIN: C;	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX
1780	1agd	A	25	274	0			322.00	B*0801; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HIV-1 GAG PEPTIDE (GGKKKYKL - INDEX PEPTIDE);	HISTOCOMPATIBILITY COMPLEX B8; B2M; PEPTIDE HLA B8, HIV, MHC CLASS I, HISTOCOMPATIBILITY COMPLEX

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1780	1bd2	E	197	283	1.2e-06	-0.26	0.90		CHAIN: C; HLA-A 0201; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; TAX PEPTIDE; CHAIN: C; T CELL RECEPTOR ALPHA; CHAIN: D; T CELL RECEPTOR BETA; CHAIN: E;	COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR) HLA A2 HEAVY CHAIN; COMPLEX (MHC/VIRAL PEPTIDE/RECEPTOR)
1780	1ed3	A	11	174	1.4e-78			128.96	CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A; D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (13N3E); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1780	1ed3	A	25	273	0	0.44	1.00		CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (13N3E); CHAIN: C, F;	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1780	1ed3	A	25	273	0			306.45	CLASS I MAJOR HISTOCOMPATIBILITY ANTIGEN RT1-AA; CHAIN: A, D; BETA-2-MICROGLOBULIN; CHAIN: B, E; PEPTIDE MTF-E (13N3E); CHAIN:	IMMUNE SYSTEM MAJOR HISTOCOMPATIBILITY COMPLEX, RAT MINOR 2 HISTOCOMPATIBILITY COMPLEX, MHC, IMMUNOLOGY, PEPTIDE 3 ANTIGEN PRESENTATION, CELLULAR IMMUNITY, CELL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									C, F;	SURFACE 4 RECEPTOR, T CELL RECEPTOR LIGAND
1780	1efx	A	11	174	5.6e-76			129.79	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1780	1efx	A	25	276	0	0.51	1.00		HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1780	1efx	A	25	276	0			332.02	HLA-CW3 (HEAVY CHAIN); CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; PEPTIDE FROM IMPORTIN ALPHA-2; CHAIN: C; NATURAL KILLER CELL RECEPTOR KIR2DL2; CHAIN: D, E;	IMMUNE SYSTEM MHC, HLA, CLASS I, KIR, NK CELL RECEPTOR, IMMUNOGLOBULIN 2 FOLD, RECEPTOR/MHC COMPLEX
1780	1elr	A	89	217	4.2e-22			52.69	TPR2A-DOMAIN OF HOP; CHAIN: A; HSP90-PEPTIDE MEEVD;	CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSP90, 2 PROTEIN

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1780	1elw	A	86	204	1.3e-26			61.34	CHAIN: B; TPR1-DOMAIN OF HOP; CHAIN: A, B; HSC70-PEPTIDE; CHAIN: C, D;	BINDING CHAPERONE HOP, TPR-DOMAIN, PEPTIDE-COMPLEX, HELICAL REPEAT, HSC70, 2 HSP70, PROTEIN BINDING
1780	1f3o	A	1	199	1.4e-48			51.22	HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CHAIN: A;	STRUCTURAL GENOMICS TRANSPORTER
1780	1fzk	A	11	174	8.4e-75			118.23	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC
1780	1fzk	A	25	272	0	0.59	1.00		H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC
1780	1fzk	A	25	272	0			293.35	H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, K-B CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; NUCLEOCAPSID PROTEIN; CHAIN: P;	IMMUNE SYSTEM SEV9; MAJOR HISTOCOMPATIBILITY COMPLEX PEPTIDE-MHC
1780	1hoc	A	11	174	5.6e-74			121.28	HISTOCOMPATIBILITY ANTIGEN MURINE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D═B═, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1780	1hoc	A	25	270	0			293.21	HISTOCOMPATIBILITY ANTIGEN MURINE CLASS I MAJOR HISTOCOMPATIBILITY COMPLEX CONSISTING 1HOC 3 OF H-2D═B═, B2-MICROGLOBULIN, AND A 9-RESIDUE PEPTIDE 1HOC 4	
1780	1hsa	A	11	174	5.6e-74			125.78	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705$ 1HSA 4	
1780	1hsa	A	25	274	0	0.67	1.00		HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-B(ASTERISK)2705$ 1HSA 4	
1780	1hsa	A	25	274	0			324.99	HISTOCOMPATIBILITY ANTIGEN HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN 1HSA 3 /HLA-	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									B(ASTERISK)2705$ 1HSA 4	
1780	1hsb	A	11	174	1.4e-75			118.41	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1780	1hsb	A	25	268	0			299.60	HISTOCOMPATIBILITY ANTIGEN CLASS I HISTOCOMPATIBILITY ANTIGEN AW68.1 (LEUCOCYTE 1HSB 3 ANTIGEN) 1HSB 4	
1780	1i4f	A	11	174	2.8e-74			129.54	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1780	1i4f	A	25	273	0	0.55	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED ANTIGEN
1780	1i4f	A	25	273	0			324.98	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN, A-2 CHAIN: A; BETA-2-MICROGLOBULIN;	IMMUNE SYSTEM MAGE-4 ANTIGEN; MAJOR HISTOCOMPATIBILITY COMPLEX, HUMAN LEUKOCYTE ANTIGEN, 2 MELANOMA-ASSOCIATED

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B; MELANOMA-ASSOCIATED ANTIGEN 4; CHAIN: C;	ANTIGEN
1780	1iam		182	282	8.4e-07	0.08	-0.03		INTERCELLULAR ADHESION MOLECULE-1; CHAIN: NULL;	RHINOVIRUS RECEPTOR ICAM-1, CD54; RHINOVIRUS RECEPTOR, CELL ADHESION, INTEGRIN LIGAND, 2 GLYCOPROTEIN, LFA-1 LIGAND, IMMUNOGLOBULIN FOLD, 3 TRANSMEMBRANE
1780	1ld9	A	11	174	1.3e-75			125.09	MHC CLASS I H-2LD HEAVY CHAIN; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; NANO-PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX LD; MAJOR HISTOCOMPATIBILITY COMPLEX, LD
1780	1ld9	A	25	266	0			287.52	MHC CLASS I H-2LD HEAVY CHAIN; CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; NANO-PEPTIDE; CHAIN: C;	MAJOR HISTOCOMPATIBILITY COMPLEX LD; MAJOR HISTOCOMPATIBILITY COMPLEX, LD
1780	1mco	H	193	283	0.0072	0.44	0.30		IMMUNOGLOBULIN IMMUNOGLOBULIN G1 (IGG1) (MCG) WITH A HINGE DELETION 1MCO 3	
1780	1mhc	A	11	174	1.4e-62			92.09	MHC CLASS I ANTIGEN H2-M3; 1MHC 6 CHAIN: A, B, D, E; 1MHC 7 NONAPEPTIDE FROM RAT NADH DEHYDROGENASE; 1MHC 12 CHAIN: C, F; 1MHC 13	HISTOCOMPATIBILITY ANTIGEN/PEPTIDE MAJOR HISTOCOMPATIBILITY COMPLEX; 1MHC 8 ND1; 1MHC 15
1780	1mhc	A	25	274	2.8e-98			274.19	MHC CLASS I ANTIGEN	HISTOCOMPATIBILITY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR TAA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									H2-M3; 1MHC 6 CHAIN: A, B, D, E; 1MHC 7 NONAPEPTIDE FROM RAT NADH DEHYDROGENASE; 1MHC 12 CHAIN: C, F; 1MHC 13	ANTIGEN/PEPTIDE MAJOR HISTOCOMPATIBILITY COMPLEX; 1MHC 8 ND1; 1MHC 15
1780	1mhe	A	12	174	4.2e-72			124.46	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-
1780	1mhe	A	26	272	0	0.34	1.00		HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON-
1780	1mhe	A	26	272	0			321.02	HLA CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-E; CHAIN: A, C; BETA-2-MICROGLOBULIN; CHAIN: B, D; PEPTIDE (VMAPRTVLL); CHAIN: P, Q;	MAJOR HISTOCOMPATIBILITY COMPLEX MHC NONCLASSICAL CHAIN, MHC-E, HLA-E, MHC CLASS HLA-E, HLA E, MAJOR HISTOCOMPATIBILITY COMPLEX, MHC, HLA, 2 BETA 2 MICROGLOBULIN, PEPTIDE, LEADER PEPTIDE, 3 NON- CLASSICAL MHC, CLASS IB MHC
1780	1qo3	A	12	174	1.4e-74			120.50	MHC CLASS I H-2DD	COMPLEX (NK RECEPTOR/MHC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1780	1qo3	A	26	272	0	0.60	1.00		MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1780	1qo3	A	26	273	0			299.18	MHC CLASS I H-2DD HEAVY CHAIN; CHAIN: A; BETA-2-MICROGLOBULIN; CHAIN: B; HIV ENVELOPE GLYCOPROTEIN 120 PEPTIDE; CHAIN: P; LY49A; CHAIN: C, D;	COMPLEX (NK RECEPTOR/MHC CLASS I) H-2 CLASS I HISTOCOMPATIBILITY ANTIGEN, B2M; NK-CELL SURFACE GLYCOPROTEIN YE1/48, NK CELL, INHIBITORY RECEPTOR, MHC-I, C-TYPE LECTIN-LIKE, 2 HISTOCOMPATIBILITY, B2M, LY49, LY-49
1780	1qqd	A	12	174	2.8e-74			127.23	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1780	1qqd	A	26	272	0	0.55	1.00		HISTOCOMPATIBILITY	IMMUNE SYSTEM

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1780	1qqd	A	26	272	0			321.09	HISTOCOMPATIBILITY LEUKOCYTE ANTIGEN (HLA)-CW4 CHAIN: A; BETA-2 MICROGLOBULIN; CHAIN: B; HLA-CW4 SPECIFIC PEPTIDE; CHAIN: C;	IMMUNE SYSTEM IMMUNOGLOBULIN (IG)-LIKE DOMAIN, ALPHA HELIX, BETA SHEET, 2 IMMUNE SYSTEM
1780	1tmc	A	11	174	1.4e-75			164.71	HISTOCOMPATIBILITY ANTIGEN TRUNCATED HUMAN CLASS I HISTOCOMPATIBILITY ANTIGEN HLA-AW68 1TMC 3 COMPLEXED WITH A DECAMERIC PEPTIDE (EVAPPEYHRK) 1TMC 4	
1782	1b0u	A	426	619	7e-41	0.52	1.00		HISTIDINE PERMEASE; CHAIN: A;	TRANSPORT PROTEIN ABC TRANSPORTER, HISP; ABC TRANSPORTER, HISTIDINE PERMEASE, TRANSPORT PROTEIN
1782	1cex		624	775	6e-09	0.61	-0.19		CUTINASE; CHAIN: NULL;	SERINE ESTERASE HYDROLASE, SERINE ESTERASE, GLYCOPROTEIN
1782	1d6j	A	446	536	0.0041	0.00	0.05		ADENOSINE-5'PHOSPHOSULFATE KINASE; CHAIN: A, B;	TRANSFERASE APS KINASE; APS KINASE, ADENYLYLSULFATE KINASE, SULFATE, NUCLEOTIDE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										2 KINASE, TRANSFERASE
1782	1e69	A	447	616	2.4e-07	-0.04	0.04		CHROMOSOME SEGREGATION SMC PROTEIN; CHAIN: A, B, C, D, E, F;	CHROMOSOME SEGREGATION SMC, STRUCTURAL MAINTENANCE OF CHROMOSOMES, COILED COIL
1782	1ex7	A	451	477	0.0055	-0.66	0.24		GUANYLATE KINASE; CHAIN: A;	TRANSFERASE GUANYLATE KINASE, SUBSTRATE-INDUCED FIT, DOMAIN MOVEMENT, 2 GMP, ATP, SUBSTRATE SPECIFICITY, X-RAY DIFFRACTION
1782	1f3o	A	421	619	2.8e-48	0.52	1.00		HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CHAIN: A;	STRUCTURAL GENOMICS TRANSPORTER
1782	1f3o	A	438	620	6e-22	0.55	1.00		HYPOTHETICAL ABC TRANSPORTER ATP-BINDING PROTEIN CHAIN: A;	STRUCTURAL GENOMICS TRANSPORTER
1782	1fuu	B	445	599	0.0096	-0.08	0.10		YEAST INITIATION FACTOR 4A; CHAIN: A, B;	TRANSLATION EUKARYOTIC INITIATION FACTOR 4A; IF4A, HELICASE, DEAD-BOX PROTEIN
1782	1g29	1	423	614	9.8e-49	0.36	1.00		MALTOSE TRANSPORT PROTEIN MALK; CHAIN: 1, 2;	SUGAR BINDING PROTEIN MALK; ATPASE, ACTIVE TRANSPORT, MALTOSE UPTAKE AND REGULATION
1782	1g6h	A	419	614	2.4e-20	0.44	1.00		HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID CHAIN: A	TRANSPORT PROTEIN BETA-CORE DOMAIN, ABC SPECIFIC-BETA-STRAND DOMAIN ALPHA-2 HELIX DOMAIN
1782	1g6h	A	432	619	2.8e-30	0.47	0.69		HIGH-AFFINITY BRANCHED-CHAIN AMINO ACID CHAIN: A	TRANSPORT PROTEIN BETA-CORE DOMAIN, ABC SPECIFIC-BETA-STRAND DOMAIN ALPHA-2 HELIX DOMAIN
1782	1g6o	A	412	536	1.2e-08	-0.08	0.00		CAG-ALPHA; CHAIN: A,	HYDROLASE TRAFFIC ATPASE;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									B;	ATPASE, TYPE IV SECRETION SYSTEM
1782	1ga6	A	624	763	9.6e-10	0.82	-0.19		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPEPSIN, PEPSTATIN-INSENSITIVE SERINE-CARBOXYL PROTEINASE
1782	1ga6	A	632	773	3.6e-09	0.65	-0.18		SERINE-CARBOXYL PROTEINASE; CHAIN: A; FRAGMENT OF TYROSTATIN; CHAIN: I;	HYDROLASE PSCP, PSEUDOMONAPEPSIN, PEPSTATIN-INSENSITIVE SERINE-CARBOXYL PROTEINASE
1782	1hey		450	543	0.0031	0.10	0.62		CHEMOTAXIS CHEY MUTANT WITH ASP 12 REPLACED BY GLY, ASP 13 REPLACED BY 1HEY 3 ASN, PHE 14 REPLACED BY GLY, SER 15 REPLACED BY GLY, MET 17 1HEY 4 REPLACED BY GLY, ARG 18 REPLACED BY LYS, ARG 19 REPLACED BY 1HEY 5 SER, ILE 20 REPLACED BY THR, GLU 35 REPLACED BY ASP (D12G, 1HEY 6 D13N,F14G,S15G,M17G,R18K,R19S,I20T,E35D) (SYNCHROTRON X-RAY 1HEY 7 DIFFRACTION) 1HEY 8		
1782	1kap	P	623	772	1.2e-06	1.06	-0.19		ALKALINE PROTEASE; 1KAP 4 CHAIN: P; 1KAP 5 TETRAPEPTIDE (GLY SER ASN SER); 1KAP 9 CHAIN: I; 1KAP 10	ZINC METALLOPROTEASE P. AERUGINOSA ALKALINE PROTEASE; 1KAP 6 CALCIUM BINDING PROTEIN 1KAP 19

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1782	1qq4	A	607	760	1.2e-08	0.83	-0.20		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1782	1qq4	A	668	774	2.4e-09	0.98	-0.19		ALPHA-LYTIC PROTEASE; CHAIN: A;	HYDROLASE DOUBLE BETA BARREL, BACTERIAL SERINE PROTEASE
1782	1tal		627	774	4.8e-09	0.81	-0.19		ALPHA-LYTIC PROTEASE; CHAIN: NULL;	SERINE PROTEASE SERINE PROTEASE, LOW TEMPERATURE, HYDROLASE, 2 SERINE PROTEINASE
1782	2por		626	760	3.6e-07	0.83	-0.19		INTEGRAL MEMBRANE PROTEIN PORIN PORIN (CRYSTAL FORM B) 2POR 3	
1782	3prn		625	780	1.2e-06	0.88	-0.19		PORIN; CHAIN: NULL;	MEMBRANE PROTEIN INTEGRAL MEMBRANE PROTEIN, PORIN, PORE EYELET MUTANT
1784	1qho	A	1022	1129	0.0039	0.39	0.11		ALPHA-AMYLASE; CHAIN: A;	HYDROLASE "MALTOGENIC" ALPHA AMYLASE; AMYLASE, GLYCOSIDE HYDROLASE, STARCH DEGRADATION
1784	1wer		1885	2041	3.6e-32	-0.23	0.07		P120GAP; CHAIN: NULL;	GTPASE ACTIVATION GAP-334, GAPETTE; GTPASE ACTIVATION, RAS, GAP, SIGNAL TRANSDUCTION, GROWTH 2 REGULATION, CANCER
1786	1a4y	A	192	638	8.4e-42	0.23	0.90		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1786	1a4y	A	324	677	6e-32	0.07	0.42		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1786	1a4y	A	350	677	4.2e-20	-0.18	0.30		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1786	1a4y	A	407	730	7e-17	-0.38	0.09		RIBONUCLEASE INHIBITOR; CHAIN: A, D; ANGIOGENIN; CHAIN: B, E;	COMPLEX (INHIBITOR/NUCLEASE) COMPLEX (INHIBITOR/NUCLEASE), COMPLEX (RI-ANG), HYDROLASE 2 MOLECULAR RECOGNITION, EPITOPE MAPPING, LEUCINE-RICH 3 REPEATS
1786	1a9n	A	133	278	1.2e-15	-0.37	0.19		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	A	149	312	3.6e-18	0.03	-0.12		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	A	385	495	1.2e-19	-0.17	0.72		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B'';	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: B, D;	SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	A	404	575	4.8e-23	0.33	0.81		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	A	438	614	8.4e-18	0.02	-0.09		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	A	524	676	2.4e-20	0.15	0.62		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	C	130	276	9.6e-15	-0.12	0.09		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	C	384	490	2.4e-19	0.15	0.82		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	C	404	583	2.4e-24	0.33	0.78		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1a9n	C	524	676	1.2e-20	0.06	0.47		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B"; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1786	1d0b	A	132	332	4.8e-16	0.39	0.90		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	189	442	2.4e-18	0.29	0.34		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1786	1d0b	A	211	391	1.4e-21	-0.15	0.83		INTERNALIN B; CHAIN: A;	CELL ADHESION
1786	1d0b	A	239	490	3.6e-21	0.09	0.76		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	248	441	1.4e-21	0.21	0.22		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	332	505	2.8e-25	0.44	1.00		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	369	554	1.2e-22	-0.07	0.06		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	36	273	4.2e-19	0.16	0.03		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	428	605	2.8e-22	0.06	0.78		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	461	676	7.2e-25	0.14	0.69		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	494	651	7e-24	0.28	0.96		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	521	678	1.4e-23	0.13	0.17		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1786	1d0b	A	566	698	8.4e-18	0.08	0.25		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1786	1dce	A	187	278	1.3e-09	0.59	0.37		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1786	1dce	A	354	444	1.4e-08	0.22	0.05		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1786	1dce	A	435	556	9.8e-10	0.13	0.37		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1786	1dce	A	483	581	1.1e-10	-0.23	0.25		RAB GERANYLGERANYLTRA NSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRA NSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1786	1dce	A	572	678	9.8e-12	-0.08	0.22		RAB GERANYLGERANYLTRA NSFERASE ALPHA	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERAS

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1786	1dce	A	625	729	7e-08	0.02	0.36		SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D; RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	E, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1786	1ds9	A	141	278	2.4e-18	-0.25	0.18		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1ds9	A	257	414	1.4e-08	-0.29	0.40		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1ds9	A	354	486	2.8e-11	-0.09	0.29		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1ds9	A	404	537	1.2e-19	-0.52	0.98		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1ds9	A	465	650	8.4e-15	-0.51	0.05		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1ds9	A	556	677	8.4e-13	-0.28	0.11		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1ds9	A	581	702	2.8e-11	-0.21	0.49		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1786	1fo1	A	454	511	1.4e-06	-0.61	0.18		NUCLEAR RNA EXPORT FACTOR 1; CHAIN: A, B;	RNA BINDING PROTEIN TAP (NFX1); RIBONUCLEOPROTEIN (RNP,RBD OR RRM) AND LEUCINE-RICH-REPEAT 2 (LRR)
1786	1fqv	A	133	274	2.4e-10	0.12	0.49		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1786	1fqv	A	167	443	7.2e-11	0.06	0.15		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1786	1fqv	A	244	481	5.6e-14	0.18	-0.01		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1786	1fqv	A	361	623	4.2e-14	0.12	0.71		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1786	1fqv	A	5	216	4.2e-09	0.12	-0.19		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1786	1ft8	A	454	511	1.4e-06	-0.38	0.07		TIP ASSOCIATING PROTEIN; CHAIN: A, B, C, D, E;	RNA BINDING PROTEIN TAP; RIBONUCLEOPROTEIN (RNP, RRM, RBD) AND LEUCINE-RICH-REPEAT 2 (LRR) DOMAINS
1786	1fyv	A	777	932	1.4e-53	0.46	1.00		TOLL-LIKE RECEPTOR 1; CHAIN: A;	SIGNALING PROTEIN BETA-ALPHA-BETA FOLD PARALLEL BETA SHEET
1786	1fyx	A	789	932	5.6e-44	0.40	1.00		TOLL-LIKE RECEPTOR 2; CHAIN: A;	SIGNALING PROTEIN BETA-ALPHA-BETA FOLD
1786	1yrg	A	113	390	1.4e-10	0.17	-0.12		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1786	1yrg	A	402	677	2.4e-29	-0.05	0.22		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1786	2bnh		134	493	3.6e-31	-0.11	0.09		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1786	2bnh		246	656	8.4e-37	-0.00	0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1786	2bnh		391	730	1.1e-17	-0.15	0.57		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1786	2bnh		8	431	1.4e-19	0.12	-0.03		RIBONUCLEASE INHIBITOR; CHAIN: NULL;	ACETYLATION RNASE INHIBITOR, RIBONUCLEASE/ANGIOGENIN INHIBITOR ACETYLATION, LEUCINE-RICH REPEATS
1792	1auk		554	657	3.6e-15	-0.19	0.17		ARYLSULFATASE A; CHAIN: NULL;	HYDROLASE CEREBROSIDE-3-SULFATE-SULFATASE; CEREBROSIDE-3-SULFATE HYDROLYSIS, LYSOSOMAL ENZYME, 2 HYDROLASE
1792	1dpi		837	921	9.8e-35	-0.32	0.93		NUCLEOTIDYLTRANSFE	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									RASE /DNA$ POLYMERASE I (KLENOW FRAGMENT) (E.C.2.7.7.7) - D/CMP 1DPI 4 COMPLEX 1DPI 5	
1792	1fsu		548	691	6e-13	-0.22	0.19		N-ACETYLGALACTOSAMINE-4-SULFATASE; CHAIN: NULL;	HYDROLASE ARYLSULFATASE B, ASB, 4-SULFATASE; SULFATASE, GLYCOSAMINOGLYCAN DEGRADATION, HYDROLASE, SIGNAL, 2 GLYCOPROTEIN, LYSOSOME
1792	1fsu		591	630	0.0013	-0.02	0.22		N-ACETYLGALACTOSAMINE-4-SULFATASE; CHAIN: NULL;	HYDROLASE ARYLSULFATASE B, ASB, 4-SULFATASE; SULFATASE, GLYCOSAMINOGLYCAN DEGRADATION, HYDROLASE, SIGNAL, 2 GLYCOPROTEIN, LYSOSOME
1792	2kfn	A	837	921	9.8e-35	0.25	1.00		KLENOW FRAGMENT; CHAIN: A; DEOXYRIBO-3'-S-PHOSPHOROTHIOLATE DNA; CHAIN: B;	COMPLEX (POLYMERASE/DNA) LARGE FRAGMENT; COMPLEX (POLYMERASE/DNA), EXONUCLEASE
1796	1a9n	A	284	415	2.4e-16	0.18	0.23		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1796	1a9n	C	284	402	8.4e-16	0.25	-0.07		U2 RNA HAIRPIN IV; CHAIN: Q, R; U2 A'; CHAIN: A, C; U2 B''; CHAIN: B, D;	COMPLEX (NUCLEAR PROTEIN/RNA) COMPLEX (NUCLEAR PROTEIN/RNA), RNA, SNRNP,RIBONUCLEOPROTEIN
1796	1d0b	A	128	320	8.4e-19	0.12	0.01		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1796	1d0b	A	200	368	4.8e-11	0.40	1.00		INTERNALIN B; CHAIN:	CELL ADHESION LEUCINE RICH

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									A;	REPEAT, CALCIUM BINDING, CELL ADHESION
1796	1d0b	A	244	417	9.8e-21	0.19	0.62		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1796	1d0b	A	309	466	1.4e-23	0.13	0.12		INTERNALIN B; CHAIN: A;	CELL ADHESION LEUCINE RICH REPEAT, CALCIUM BINDING, CELL ADHESION
1796	1dce	A	200	383	3.6e-10	0.13	-0.18		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1796	1dce	A	292	399	1.1e-10	0.50	0.98		RAB GERANYLGERANYLTRANSFERASE ALPHA SUBUNIT; CHAIN: A, C; RAB GERANYLGERANYLTRANSFERASE BETA SUBUNIT; CHAIN: B, D;	TRANSFERASE CRYSTAL STRUCTURE, RAB GERANYLGERANYLTRANSFERASE, 2.0 A 2 RESOLUTION, N-FORMYLMETHIONINE, ALPHA SUBUNIT, BETA SUBUNIT
1796	1ds9	A	295	368	3.6e-11	-0.57	0.13		OUTER ARM DYNEIN; CHAIN: A;	CONTRACTILE PROTEIN LEUCINE-RICH REPEAT, BETA-BETA-ALPHA CYLINDER, DYNEIN, 2 CHLAMYDOMONAS, FLAGELLA
1796	1ev2	E	437	528	4.8e-07	0.28	0.96		FIBROBLAST GROWTH FACTOR 2; CHAIN: A, B, C, D; FIBROBLAST GROWTH FACTOR RECEPTOR 2; CHAIN: E, F, G, H;	GROWTH FACTOR/GROWTH FACTOR RECEPTOR FGF2; FGFR2; IMMUNOGLOBULIN (IG)LIKE DOMAINS BELONGING TO THE I-SET 2 SUBGROUP WITHIN IG-LIKE DOMAINS, B-TREFOIL FOLD

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1796	1fhg	A	431	526	4.8e-06	0.38	0.17		TELOKIN; CHAIN: A	CONTRACTILE PROTEIN IMMUNOGLOBULIN FOLD, BETA BARREL
1796	1fqv	A	225	458	4.2e-09	-0.18	0.00		SKP2; CHAIN: A, C, E, G, I, K, M, O; SKP1; CHAIN: B, D, F, H, J, L, N, P;	LIGASE CYCLIN A/CDK2-ASSOCIATED PROTEIN P45; CYCLIN A/CDK2-ASSOCIATED PROTEIN P19; SKP1, SKP2, F-BOX, LRR, LEUCINE-RICH REPEAT, SCF, UBIQUITIN, 2 E3, UBIQUITIN PROTEIN LIGASE
1796	1ytg	A	200	382	6e-10	0.14	-0.18		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1796	1yrg	A	298	392	1.2e-07	-0.17	0.04		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1796	1yrg	A	314	580	2.8e-12	0.21	-0.15		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1796	1yrg	A	78	350	2.8e-10	0.03	-0.18		GTPASE-ACTIVATING PROTEIN RNA1_SCHPO; CHAIN: A, B;	TRANSCRIPTION RNA1P; RANGAP; GTPASE-ACTIVATING PROTEIN FOR SPI1, GTPASE-ACTIVATING PROTEIN, GAP, RNA1P, RANGAP, LRR, LEUCINE-2 RICH REPEAT PROTEIN, TWINNING, HEMIHEDRAL TWINNING, 3 MEROHEDRAL TWINNING, MEROHEDRY
1800	1ae1	A	175	345	1.4e-10	-0.12	0.09		TROPINONE REDUCTASE-I; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
1800	1ae1	B	175	347	8.4e-11	-0.11	0.03		TROPINONE REDUCTASE-I; CHAIN: A, B;	OXIDOREDUCTASE OXIDOREDUCTASE, TROPANE ALKALOID BIOSYNTHESIS, REDUCTION OF 2 TROPINONE TO TROPINE, SHORT-CHAIN DEHYDROGENASE
1800	1edo	A	179	287	5.6e-07	0.16	0.10		BETA-KETO ACYL CARRIER PROTEIN REDUCTASE; CHAIN: A;	OXIDOREDUCTASE NUCLEOTIDE FOLD, ROSSMANN FOLD
1800	1fjh	A	180	281	2.8e-06	0.12	0.78		3ALPHA-HYDROXYSTEROID DEHYDROGENASE/CARBONYL CHAIN: A, B;	OXIDOREDUCTASE 3ALPHA-HSD/CR, HYDROXYSTEROID SHORT CHAIN DEHYDROGENASE, SDR, CARBONYL REDUCTASE, STEROID, 2 HYDROXYSTEROID, XENOBIOTIC, METYRAPONE, OLIGOMERISATION, 3 COMAMONAS TESTOSTERONI

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1800	1fmc	A	175	349	2.8e-10	-0.22	0.00		7 ALPHA-HYDROXYSTEROID DEHYDROGENASE; CHAIN: A, B;	OXIDOREDUCTASE SHORT-CHAIN DEHYDROGENASE/REDUCTASE, BILE ACID CATABOLISM
1800	1i01	A	174	279	1.4e-11	0.06	0.60		BETA-KETOACYL [ACP] REDUCTASE; CHAIN: A, B, C, D, E, F, G, H;	OXIDOREDUCTASE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, 3- ROSSMAN FOLD
1800	1i01	C	174	279	5.6e-11	0.03	0.41		BETA-KETOACYL [ACP] REDUCTASE; CHAIN: A, B, C, D, E, F, G, H;	OXIDOREDUCTASE 3-OXOACYL-[ACYL-CARRIER PROTEIN] REDUCTASE, 3- ROSSMAN FOLD
1800	1jb1	A	169	212	0.00098	-0.09	0.45		HPRK PROTEIN; CHAIN: A;	TRANSFERASE/HYDROLASE CATABOLITE REPRESSION, HPR PHOSPHORYLATION, LACTOBACILLUS 2 CASEI, P-LOOP, PROTEIN KINASE, HEXAMER
1805	1ffnn	A	64	199	0.0024	0.38	0.09		CELL DIVISION CONTROL PROTEIN 6; CHAIN: A, B;	CELL CYCLE CDC6P; CDC6, CDC18, ORC1, AAA PROTEIN, DNA REPLICATION INITIATION 2 FACTOR, CELL CYCLE CONTROL FACTOR
1805	1g41	A	67	290	8.4e-11	-0.09	0.18		HEAT SHOCK PROTEIN HSLU; CHAIN: A;	CHAPERONE AAA-ATPASE, CLPY, ATP-DEPENDENT PROTEOLYSIS
1805	1im2	A	67	290	2.8e-09	0.13	-0.08		ATP-DEPENDENT HSL PROTEASE ATP-BINDING SUBUNIT CHAIN: A;	CHAPERONE HEAT SHOCK PROTEIN HSLU; CHAPERONE, AAA FAMILY
1809	1ck4	A	126	202	5.9e-05	0.08	-0.20		INTEGRIN ALPHA-1; CHAIN: A, B;	STRUCTURAL PROTEIN I-DOMAIN, METAL BINDING, COLLAGEN, ADHESION
1809	1ido		125	202	0.003	0.14	-0.20		INTEGRIN; CHAIN: NULL;	CELL ADHESION PROTEIN A-DOMAIN INTEGRIN, CELL ADHESION PROTEIN, GLYCOPROTEIN,

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										EXTRACELLULAR 2 MATRIX, CYTOSKELETON
1809	1qc5	A	125	202	0.00012	0.40	-0.20		ALPHA1 BETA1 INTEGRIN; CHAIN: A; ALPHA1 BETA1 INTEGRIN; CHAIN: B;	CELL ADHESION INTEGRIN, CELL ADHESION
1813	1a1h	A	412	507	7.5e-24	0.04	-0.20		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1813	1a1h	A	438	535	1.3e-28	0.07	-0.20		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1813	1a1h	A	739	818	3e-23	0.13	-0.20		QGSR ZINC FINGER PEPTIDE; CHAIN: A; DUPLEX OLIGONUCLEOTIDE BINDING SITE; CHAIN: B, C;	COMPLEX (ZINC FINGER/DNA) COMPLEX (ZINC FINGER/DNA), ZINC FINGER, DNA-BINDING PROTEIN
1813	1mey	C	267	332	3e-35	0.43	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)
1813	1mey	C	383	463	6e-42	0.06	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE, COMPLEX (ZINC FINGER/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1813	1mey	C	414	508	1.8e-11	0.00	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1813	1mey	C	768	846	1.5e-39	0.29	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1813	1mey	C	796	852	3e-24	0.14	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1813	1mey	G	766	793	1.2e-12	0.11	-0.20		DNA; CHAIN: A, B, D, E; CONSENSUS ZINC FINGER PROTEIN; CHAIN: C, F, G;	COMPLEX (ZINC FINGER/DNA) ZINC FINGER, PROTEIN-DNA INTERACTION, PROTEIN DESIGN, 2 CRYSTAL STRUCTURE,
1813	1ubd	C	741	846	9e-28	0.10	-0.20		YY1; CHAIN: C; ADENO-ASSOCIATED VIRUS P5 INITIATOR ELEMENT DNA; CHAIN: A, B;	COMPLEX (TRANSCRIPTION REGULATION/DNA) YING-YANG 1; TRANSCRIPTION INITIATION, INITIATOR ELEMENT, YY1, ZINC 2 FINGER PROTEIN, DNA-PROTEIN RECOGNITION, 3 COMPLEX (TRANSCRIPTION REGULATION/DNA)
1813	2adr		438	509	4.5e-13	0.15	-0.20		ADR1; CHAIN: NULL;	TRANSCRIPTION REGULATION TRANSCRIPTION REGULATION, ADR1, ZINC FINGER, NMR
1813	2gli	A	173	319	1.5e-28	0.00	-0.20		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1813	2gli	A	445	594	3e-34	0.05	-0.20		ZINC FINGER PROTEIN GLI1; CHAIN: A; DNA; CHAIN: C, D;	COMPLEX (DNA-BINDING PROTEIN/DNA) FIVE-FINGER GLI; GLI, ZINC FINGER, COMPLEX (DNA-BINDING PROTEIN/DNA)
1814	1foh	A	5	153	0.0018	0.11	-0.20		PHENOL HYDROXYLASE; CHAIN: A, B, C, D;	FLAVIN FLAVIN, PHENOL HYDROXYLASE, MONOOXYGENASE, OXIDOREDUCTASE
1815	1a0j	A	123	334	4.5e-80			77.31	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1815	1a0j	A	140	362	7.5e-86			87.11	TRYPSIN; CHAIN: A, B, C, D;	SERINE PROTEASE SERINE PROTEINASE, TRYPSIN, HYDROLASE
1815	1a0l	A	141	332	1.5e-77			103.34	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1815	1a0l	A	158	380	6e-85			111.98	BETA-TRYPTASE; CHAIN: A, B, C, D;	SERINE PROTEINASE TRYPSIN-LIKE SERINE PROTEINASE, TETRAMER, HEPARIN, ALLERGY, 2 ASTHMA
1815	1a5e		9	182	9e-25			64.19	TUMOR SUPPRESSOR P16INK4A; CHAIN: NULL;	ANTI-ONCOGENE CELL CYCLE, ANTI-ONCOGENE, REPEAT, ANK REPEAT
1815	1a5i	A	96	334	4.5e-61			76.22	PLASMINOGEN ACTIVATOR; CHAIN: A; GLU-GLY-ARG CHLOROMETHYL KETONE; CHAIN: I;	COMPLEX (SERINE PROTEASE/INHIBITOR) (DELTAFEK)DSPAALPHA1; EGRCMK; SERINE PROTEASE, FIBRINOLYTIC ENZYMES, PLASMINOGEN 2 ACTIVATORS
1815	1aut	C	137	334	1.5e-58			80.06	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA;

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1815	1aut	C	154	365	1e-70			89.76	ACTIVATED PROTEIN C; CHAIN: C, L; D-PHE-PRO-MAI; CHAIN: P;	COMPLEX (BLOOD COAGULATION/INHIBITOR) AUTOPROTHROMBIN IIA; HYDROLASE, SERINE PROTEINASE), PLASMA CALCIUM BINDING, 2 GLYCOPROTEIN, COMPLEX (BLOOD COAGULATION/INHIBITOR)
1815	1awc	B	22	168	7.5e-40			71.90	GA BINDING PROTEIN ALPHA; CHAIN: A; GA BINDING PROTEIN BETA 1; CHAIN: B; DNA; CHAIN: D, E;	COMPLEX (TRANSCRIPTION REGULATION/DNA) GABPALPHA; GABPBETA1; COMPLEX (TRANSCRIPTION REGULATION/DNA), DNA-BINDING, 2 NUCLEAR PROTEIN, ETS DOMAIN, ANKYRIN REPEATS, TRANSCRIPTION 3 FACTOR
1815	1bd8		1	154	9e-30			71.86	P19INK4D CDK4/6 INHIBITOR; CHAIN: NULL;	TUMOR SUPPRESSOR TUMOR SUPPRESSOR, CDK4/6 INHIBITOR, ANKYRIN MOTIF
1815	1bi7	B	22	152	6e-25			61.32	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; MULTIPLE TUMOR SUPPRESSOR; CHAIN: B;	COMPLEX (KINASE/ANTI-ONCOGENE) CDK6; P16INK4A, MTS1; CYCLIN DEPENDENT KINASE, CYCLIN DEPENDENT KINASE INHIBITORY 2 PROTEIN, CDK, INK4, CELL CYCLE, MULTIPLE TUMOR SUPPRESSOR, 3 MTS1, COMPLEX (KINASE/ANTI-ONCOGENE) HEADER
1815	1bio		140	379	7.5e-61			85.15	COMPLEMENT FACTOR	SERINE PROTEASE SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STARTAA	ENDAA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									D; CHAIN: NULL;	PROTEASE, HYDROLASE, COMPLEMENT, FACTOR D, CATALYTIC 2 TRIAD, SELF-REGULATION
1815	1b1x	B	2	153	3e-29			64.53	CYCLIN-DEPENDENT KINASE 6; CHAIN: A; P19INK4D; CHAIN: B;	COMPLEX (INHIBITOR PROTEIN/KINASE) INHIBITOR PROTEIN, CYCLIN-DEPENDENT KINASE, CELL CYCLE 2 CONTROL, ALPHA/BETA, COMPLEX (INHIBITOR PROTEIN/KINASE)
1815	1bru	P	116	334	9e-71			80.45	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1815	1bru	P	133	380	3e-79			93.17	ELASTASE; CHAIN: P;	SERINE PROTEASE PPE; SERINE PROTEASE, HYDROLASE
1815	1bu9	A	20	200	1.5e-35			66.00	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A;	HORMONE/GROWTH FACTOR P18-INK4C; CELL CYCLE INHIBITOR, P18INK4C, TUMOR, SUPPRESSOR, CYCLIN- 2 DEPENDENT KINASE, HORMONE/GROWTH FACTOR
1815	1c5y	B	139	362	1.5e-71			85.63	UROKINASE-TYPE PLASMINOGEN ACTIVATOR; CHAIN: A; UROKINASE-TYPE PLASMINOGEN ACTIVATOR; CHAIN: B;	BLOOD CLOTTING SELECTIVE, S1 SITE INHIBITOR, STRUCTURE-BASED DRUG DESIGN, 2 UROKINASE, TRYPSIN, THROMBIN
1815	1cgh	A	120	334	6e-55			82.82	CATHEPSIN G; CHAIN: A; PHOSPHONATE INHIBITOR SUC-VAL-PRO-PHEP-(OPH)2; CHAIN: S;	COMPLEX (SERINE PROTEASE/INHIBITOR) INFLAMMATION, INHIBITOR, SPECIFICITY, SERINE PROTEASE, 2 COMPLEX (SERINE PROTEASE/INHIBITOR)
1815	1cgh	A	137	361	3e-54			88.26	CATHEPSIN G; CHAIN:	COMPLEX (SERINE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									A; PHOSPHONATE INHIBITOR SUC-VAL-PRO-PHEP-(OPH)2; CHAIN: S;	PROTEASE/INHIBITOR) INFLAMMATION, INHIBITOR, SPECIFICITY, SERINE PROTEASE, 2 COMPLEX (SERINE PROTEASE/INHIBITOR)
1815	1chg		102	334	1.5e-66			83.30	HYDROLASE ZYMOGEN (SERINE PROTEINASE) CHYMOTRYPSINOGEN A 1CHG 4	
1815	1chg		119	376	4.5e-70			92.78	HYDROLASE ZYMOGEN (SERINE PROTEINASE) CHYMOTRYPSINOGEN A 1CHG 4	
1815	1d6w	A	78	334	6e-64			76.95	THROMBIN; CHAIN: A; DECAPEPTIDE INHIBITOR; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR HYDROLASE, THROMBIN, THROMBIN INHIBITOR
1815	1dan	H	123	334	6e-64			82.55	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T; U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1815	1dan	H	140	383	3e-73			101.34	BLOOD COAGULATION FACTOR VIIA; CHAIN: L, H; SOLUBLE TISSUE FACTOR; CHAIN: T, U; D-PHE-PHE-ARG-CHLOROMETHYLKETONE (DFFRCMK) WITH CHAIN: C;	BLOOD COAGULATION, SERINE PROTEASE, COMPLEX, CO-FACTOR, 2 RECEPTOR ENZYME, INHIBITOR, GLA, EGF, 3 COMPLEX (SERINE PROTEASE/COFACTOR/LIGAND)
1815	1ddj	A	106	334	7.5e-74			89.66	PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	STAR T AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										DOMAIN
1815	1ddj	A	123	362	9e-81			97.69	PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
1815	1ddj	A	125	380	9e-81	0.07	-0.20		PLASMINOGEN; CHAIN: A, B, C, D;	BLOOD CLOTTING PLASMINOGEN, CATALYTIC DOMAIN
1815	1dlk	B	116	334	6e-70			90.13	DELTA-CHYMOTRYPSIN; CHAIN: A, C; DELTA-CHYMOTRYPSIN; CHAIN: B, D;	HYDROLASE DELTA-CHYMOTRYPSIN, PEPTIDIC INHIBIOR, CHLOROMETHYL KETONE
1815	1dlk	B	140	376	1.2e-73			101.03	DELTA-CHYMOTRYPSIN; CHAIN: A, C; DELTA-CHYMOTRYPSIN; CHAIN: B, D;	HYDROLASE DELTA-CHYMOTRYPSIN, PEPTIDIC INHIBIOR, CHLOROMETHYL KETONE
1815	1doj	A	73	334	4.5e-63			80.24	ALPHA-THROMBIN; CHAIN: A; HIRUGEN; CHAIN: B; RWJ-51438; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR THROMBIN, SERINE PROTEASE, ENZYME INHIBITION
1815	1doj	A	90	382	7.5e-71			92.95	ALPHA-THROMBIN; CHAIN: A; HIRUGEN; CHAIN: B; RWJ-51438; CHAIN: I;	HYDROLASE/HYDROLASE INHIBITOR THROMBIN, SERINE PROTEASE, ENZYME INHIBITION
1815	1ekb	B	112	334	3e-72			97.69	ENTEROPEPTIDASE; CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	HYDROLASE/HYDROLASE INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR
1815	1ekb	B	129	369	1.5e-79			104.93	ENTEROPEPTIDASE;	HYDROLASE/HYDROLASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									CHAIN: A; ENTEROPEPTIDASE; CHAIN: B; VAL-ASP-ASP-ASP-ASP-LYS PEPTIDE; CHAIN: C;	INHIBITOR ENTEROKINASE, HEAVY CHAIN; ENTEROKINASE, LIGHT CHAIN; ENTEROPEPTIDASE, TRYPSINOGEN ACTIVATION, 2 HYDROLASE/HYDROLASE INHIBITOR
1815	1elt		131	377	3e-73			84.92	ELASTASE; 1ELT 4 CHAIN; NULL; 1ELT 5	SERINE PROTEINASE
1815	1euf	A	120	334	1.5e-62			76.49	DUODENASE; CHAIN: A;	HYDROLASE BOVINE DUODENASE, SERINE PROTEASE, DUAL SPECIFICITY, 2 CRYSTAL STRUCTURE
1815	1fi8	A	120	334	1.5e-59			88.45	NATURAL KILLER CELL PROTEASE 1; CHAIN: A, B; ECOTIN; CHAIN: C, E; ECOTIN; CHAIN: D, F;	HYDROLASE/HYDROLASE INHIBITOR GRANZYME B; COMPLEX (SERINE PROTEASE/INHIBITOR), PROTEASE SUBSTRATE 2 INTERACTIONS, BETA STRAND STRUCTURE, CHYMOTRYPSIN FOLD, 3 GRANZYME B, ECOTIN
1815	1fi8	A	137	361	1.5e-60			94.52	NATURAL KILLER CELL PROTEASE 1; CHAIN: A, B; ECOTIN; CHAIN: C, E; ECOTIN; CHAIN: D, F;	HYDROLASE/HYDROLASE INHIBITOR GRANZYME B; COMPLEX (SERINE PROTEASE/INHIBITOR), PROTEASE SUBSTRATE 2 INTERACTIONS, BETA STRAND STRUCTURE, CHYMOTRYPSIN FOLD, 3 GRANZYME B, ECOTIN
1815	1fiw	A	106	334	3e-68			77.63	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
1815	1fiw	A	123	371	3e-74			93.93	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-	HYDROLASE ANTI-PARALLEL BETA-BARREL

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									ACROSIN LIGHT CHAIN; CHAIN: L	
1815	1fiz	A	103	334	9e-69			78.10	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
1815	1fiz	A	120	392	3e-75			94.78	BETA-ACROSIN HEAVY CHAIN; CHAIN: A; BETA-ACROSIN LIGHT CHAIN; CHAIN: L	HYDROLASE ANTI-PARALLEL BETA-BARREL
1815	1fmi	A	132	334	7.5e-79			79.05	TRYPSIN; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
1815	1fmi	A	140	365	3e-86			89.59	TRYPSIN; CHAIN: A;	HYDROLASE SERINE PROTEASE, HYDROLASE
1815	1fxy	A	123	334	3e-69			77.08	COAGULATION FACTOR XA-TRYPSIN CHIMERA; CHAIN: A; D-PHE-PRO-ARG-CHLOROMETHYLKETONE (PPACK) WITH CHAIN: I;	COMPLEX (PROTEASE/INHIBITOR) TRYPSIN, COAGULATION FACTOR XA, CHIMERA, PROTEASE, PPACK, 2 CHLOROMETHYLKETONE, COMPLEX (PROTEASE/INHIBITOR)
1815	1gct	A	113	334	1.3e-69			90.30	HYDROLASE (SERINE PROTEINASE) GAMMA-*CHYMOTRYPSIN *A (E.C.3.4.21.1) ($P*H 7.0) 1GCT 3	
1815	1gct	A	130	380	9e-74			99.87	HYDROLASE (SERINE PROTEINASE) GAMMA-*CHYMOTRYPSIN *A (E.C.3.4.21.1) ($P*H 7.0) 1GCT 3	
1815	1ihb	A	25	192	7.5e-35			64.46	CYCLIN-DEPENDENT KINASE 6 INHIBITOR; CHAIN: A, B;	CELL CYCLE INHIBITOR P18-INK4C(INK6); CELL CYCLE INHIBITOR, P18-INK4C(INK6),

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
										ANKYRIN REPEAT, 2 CDK 4/6 INHIBITOR
1815	1ikn	D	2	208	6e-40			55.70	NF-KAPPA-B P65 SUBUNIT; CHAIN: A; NF-KAPPA-B P50D SUBUNIT; CHAIN: C; I-KAPPA-B-ALPHA; CHAIN: D;	TRANSCRIPTION FACTOR P65; P50D; TRANSCRIPTION FACTOR, IKB/NFKB COMPLEX
1815	1jbu	H	143	383	1.2e-65			85.70	COAGULATION FACTOR VII; CHAIN: H; COAGULATION FACTOR VII; CHAIN: L; PEPTIDE EXOSITE INHIBITOR A-183; CHAIN: X;	HYDROLASE SERUM PROTHROMBIN CONVERSION ACCELERATOR; SERUM PROTHROMBIN CONVERSION ACCELERATOR; SHIFTED REGISTRATION, BETA-STRANDS
1815	1myo		23	142	3e-25			76.78	MYOTROPHIN; CHAIN: NULL	ANK-REPEAT MYOTROPHIN, ACETYLATION, NMR, ANK-REPEAT
1815	1nfi	E	1	200	3e-40			59.20	NF-KAPPA-B P65; CHAIN: A, C; NF-KAPPA-B P50; CHAIN: B, D; I-KAPPA-B-ALPHA; CHAIN: E, F;	COMPLEX (TRANSCRIPTION REG/ANK REPEAT) COMPLEX (TRANSCRIPTION REGULATION/ANK REPEAT), ANKYRIN 2 REPEAT HELIX
1815	1pyt	D	104	334	3e-65			86.27	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE
1815	1pyt	D	116	379	3e-71			94.42	PROCARBOXYPEPTIDASE A; CHAIN: A, B; PROPROTEINASE E; CHAIN: C; CHYMOTRYPSINOGEN C; CHAIN: D;	TERNARY COMPLEX (ZYMOGEN) TC, PCPA-TC; TERNARY COMPLEX (ZYMOGEN), SERINE PROTEINASE, C-TERMINAL 2 PEPTIDASE

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
1815	1qnj	A	114	334	1.5e-62			79.44	ELASTASE; CHAIN: A;	HYDROLASE (SERINE PROTEASE) PPE; HYDROLASE(SERINE PROTEASE), ATOMIC RESOLUTION
1815	1qnj	A	131	380	1.4e-72			90.58	ELASTASE; CHAIN: A;	HYDROLASE (SERINE PROTEASE) PPE; HYDROLASE(SERINE PROTEASE), ATOMIC RESOLUTION
1815	1rfn	A	28	148	3e-34	0.02	-0.20		COAGULATION FACTOR IX; CHAIN: A; COAGULATION FACTOR IX; CHAIN: B;	COAGULATION FACTOR SERINE PROTEINASE, BLOOD COAGULATION, COAGULATION FACTOR
1815	1rtf	B	111	334	6e-61			82.14	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
1815	1rtf	B	128	370	4.5e-72			89.37	TWO CHAIN TISSUE PLASMINOGEN ACTIVATOR; CHAIN: A, B;	SERINE PROTEASE (TC)-T-PA; SERINE PROTEASE, FIBRINOLYTIC ENZYMES
1815	1sgf	G	123	334	7.5e-71			79.09	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1815	1sgf	G	140	362	6e-79			85.83	NERVE GROWTH FACTOR; CHAIN: A, B, G, X, Y, Z;	GROWTH FACTOR 7S NGF; GROWTH FACTOR (BETA-NGF), HYDROLASE - SERINE PROTEINASE 2 (GAMMA-NGF), INACTIVE SERINE PROTEINASE (ALPHA-NGF)
1815	1tm	A	123	334	4.5e-77			77.36	HYDROLASE (SERINE PROTEINASE) TRYPSIN	

Table 5

SEQ ID NO:	PDB ID	CHAIN ID	START AA	END AA	Psi Blast	Verify score	PMF score	SEQFOLD score	Compound	PDB annotation
									(E.C.3.4.21.4) COMPLEXED WITH THE INHIBITOR 1TRN 3 DIISOPROPYL-FLUOROPHOSPHOFLUORIDATE (DFP) 1TRN 4 HUMAN TRYPSIN, DFP INHIBITED 1TRN 6	
1815	1ycs	B	25	229	7.5e-22			71.42	P53; CHAIN: A; 53BP2; CHAIN: B;	COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS) P53BP2; ANKYRIN REPEATS, SH3, P53, TUMOR SUPPRESSOR, MULTIGENE 2 FAMILY, NUCLEAR PROTEIN, PHOSPHORYLATION, DISEASE MUTATION, 3 POLYMORPHISM, COMPLEX (ANTI-ONCOGENE/ANKYRIN REPEATS)
1815	2sta	E	140	379	1.4e-85	0.04	-0.20		TRYPSIN; CHAIN: E; TRYPSIN INHIBITOR; CHAIN: I	HYDROLASE/HYDROLASE INHIBITOR SERINE PROTEINASE, TRYPSIN INHIBITOR
1817	1ds1	A	53	400	1.8e-46			52.55	CLAVAMINATE SYNTHASE 1; CHAIN: A;	OXIDOREDUCTASE,LYASE CLAVAMINIC ACID SYNTHASE 1, CAS1; OXYGENASE, TRIFUNCTIONAL ENZYME, CLAVAMINATE SYNTHASE 1

Table 6
1105

SEQ ID	Position	Maximum score	Average score
916	1-35	0.978	0.879
918	1-21	0.953	0.900
921	1-19	0.957	0.919
923	1-45	0.961	0.594
924	1-64	0.994	0.484
925	1-25	0.936	0.635
926	1-32	0.997	0.899
927	1-21	0.991	0.946
928	1-25	0.929	0.613
929	1-35	0.850	0.485
930	1-39	0.861	0.465
931	1-29	0.906	0.675
932	1-24	0.905	0.496
933	1-24	0.993	0.956
934	1-31	0.937	0.811
935	1-21	0.989	0.939
936	1-20	0.973	0.941
937	1-11	0.800	0.691
938	1-24	0.912	0.763
939	1-22	0.992	0.851
940	1-20	0.975	0.934
941	1-16	0.978	0.797
942	1-23	0.966	0.816
943	1-19	0.905	0.660
944	1-56	0.966	0.498
945	1-40	0.859	0.533
946	1-20	0.953	0.751
947	1-31	0.833	0.502
948	1-39	0.986	0.641
949	1-26	0.978	0.932
950	1-67	0.976	0.450
951	1-20	0.991	0.708
952	1-36	0.954	0.637
953	1-16	0.844	0.480
954	1-32	0.953	0.521
955	1-58	0.989	0.500
956	1-25	0.981	0.896
957	1-28	0.954	0.836
958	1-19	0.982	0.943
959	1-55	0.988	0.465
960	1-33	0.925	0.630
961	1-40	0.916	0.477
962	1-13	0.816	0.645
963	1-17	0.946	0.734
964	1-17	0.985	0.930
965	1-51	0.991	0.500
966	1-49	0.963	0.508
967	1-51	0.971	0.493
968	1-15	0.959	0.731
969	1-13	0.822	0.537
970	1-16	0.862	0.496
971	1-31	0.956	0.674
972	1-32	0.855	0.601
973	1-15	0.826	0.532
974	1-57	0.954	0.648

Table 6
1106

SEQ ID	Position	Maximum score	Average score
975	1-20	0.976	0.854
976	1-22	0.873	0.586
977	1-26	0.985	0.839
978	1-49	0.963	0.774
979	1-26	0.843	0.609
980	1-57	0.966	0.561
981	1-16	0.912	0.705
982	1-22	0.962	0.827
983	1-13	0.803	0.580
984	1-51	0.932	0.462
985	1-20	0.982	0.890
986	1-20	0.977	0.923
987	1-21	0.977	0.868
988	1-23	0.838	0.580
989	1-39	0.905	0.628
990	1-23	0.989	0.864
991	1-20	0.884	0.650
992	1-19	0.985	0.920
993	1-28	0.887	0.505
994	1-27	0.955	0.743
995	1-27	0.992	0.934
996	1-53	0.953	0.723
997	1-30	0.905	0.522
998	1-20	0.954	0.746
999	1-19	0.821	0.482
1000	1-20	0.978	0.953
1001	1-45	0.890	0.608
1037	1-31	0.921	0.630
1038	1-36	0.972	0.563
1039	1-39	0.976	0.551
1040	1-26	0.937	0.703
1041	1-74	0.991	0.543
1042	1-23	0.945	0.797
1043	1-16	0.977	0.506
1044	1-21	0.967	0.759
1045	1-22	0.861	0.539
1046	1-27	0.934	0.682
1047	1-18	0.983	0.962
1048	1-22	0.827	0.517
1049	1-34	0.980	0.703
1050	1-15	0.987	0.955
1051	1-28	0.995	0.945
1052	1-18	0.995	0.977
1053	1-25	0.935	0.739
1054	1-19	0.976	0.950
1055	1-49	0.933	0.538
1056	1-22	0.918	0.723
1057	1-25	0.972	0.902
1058	1-52	0.981	0.622
1059	1-75	0.969	0.541
1060	1-75	0.979	0.817
1061	1-22	0.957	0.756
1062	1-45	0.978	0.852
1063	1-29	0.984	0.954
1064	1-36	0.994	0.713

Table 6
1107

SEQ ID	Position	Maximum score	Average score
1065	1-34	0.914	0.608
1066	1-25	0.986	0.952
1067	1-38	0.990	0.909
1068	1-54	0.908	0.565
1069	1-20	0.870	0.708
1070	1-27	0.985	0.856
1071	1-23	0.966	0.812
1072	1-54	0.967	0.524
1160	1-36	0.948	0.776
1161	1-26	0.962	0.783
1162	1-31	0.919	0.543
1164	1-26	0.988	0.886
1166	1-53	0.998	0.751
1167	1-20	0.993	0.968
1168	1-24	0.987	0.924
1169	1-21	0.973	0.760
1170	1-56	0.962	0.585
1171	1-39	0.978	0.768
1172	1-25	0.969	0.937
1173	1-79	0.967	0.612
1174	1-23	0.990	0.934
1175	1-23	0.990	0.932
1176	1-42	0.977	0.677
1177	1-22	0.969	0.897
1178	1-17	0.869	0.641
1179	1-45	0.987	0.656
1180	1-31	0.956	0.853
1181	1-64	0.996	0.558
1182	1-50	0.986	0.566
1183	1-38	0.987	0.864
1184	1-28	0.987	0.924
1185	1-48	0.911	0.557
1186	1-58	0.914	0.462
1187	1-20	0.992	0.794
1188	1-24	0.894	0.608
1189	1-19	0.986	0.967
1190	1-23	0.965	0.817
1191	1-23	0.965	0.817
1192	1-53	0.884	0.504
1193	1-31	0.982	0.857
1194	1-18	0.805	0.583
1195	1-20	0.950	0.843
1196	1-25	0.803	0.575
1197	1-26	0.869	0.476
1198	1-23	0.982	0.866
1199	1-21	0.959	0.915
1200	1-30	0.983	0.652
1201	1-21	0.932	0.654
1202	1-21	0.932	0.654
1203	1-20	0.932	0.697
1204	1-26	0.946	0.775
1205	1-20	0.986	0.948
1206	1-64	0.865	0.475
1207	1-44	0.881	0.488
1208	1-19	0.991	0.973

Table 6
1108

SEQ ID	Position	Maximum score	Average score
1209	1-38	0.938	0.459
1210	1-17	0.954	0.741
1211	1-20	0.916	0.802
1212	1-24	0.961	0.879
1213	1-20	0.938	0.716
1214	1-19	0.959	0.752
1215	1-55	0.946	0.682
1216	1-23	0.965	0.883
1217	1-23	0.965	0.883
1218	1-21	0.909	0.693
1219	1-17	0.971	0.886
1220	1-22	0.833	0.607
1221	1-16	0.948	0.836
1222	1-27	0.968	0.788
1223	1-23	0.853	0.523
1224	1-23	0.842	0.544
1225	1-19	0.937	0.713
1226	1-47	0.947	0.637
1227	1-21	0.984	0.933
1228	1-34	0.969	0.882
1229	1-15	0.894	0.745
1230	1-26	0.966	0.760
1231	1-28	0.883	0.474
1232	1-32	0.939	0.693
1233	1-28	0.915	0.655
1234	1-28	0.990	0.959
1235	1-39	0.926	0.696
1236	1-17	0.882	0.558
1237	1-16	0.967	0.933
1238	1-19	0.942	0.799
1239	1-19	0.910	0.773
1240	1-19	0.947	0.805
1241	1-20	0.976	0.875
1242	1-20	0.976	0.875
1243	1-15	0.973	0.942
1244	1-16	0.965	0.911
1245	1-17	0.985	0.956
1246	1-21	0.883	0.620
1247	1-13	0.874	0.527
1248	1-21	0.945	0.852
1249	1-24	0.903	0.540
1250	1-26	0.959	0.786
1251	1-30	0.934	0.585
1252	1-27	0.962	0.740
1253	1-25	0.842	0.507
1254	1-19	0.965	0.797
1255	1-20	0.970	0.804
1256	1-19	0.956	0.791
1257	1-21	0.977	0.868
1258	1-23	0.932	0.770
1259	1-31	0.960	0.635
1260	1-24	0.954	0.803
1261	1-43	0.949	0.467
1262	1-28	0.951	0.667
1263	1-28	0.963	0.844

Table 6
1109

SEQ ID	Position	Maximum score	Average score
1264	1-60	0.971	0.472
1265	1-17	0.950	0.878
1266	1-22	0.984	0.852
1267	1-32	0.939	0.646
1268	1-50	0.939	0.491
1269	1-42	0.841	0.500
1270	1-23	0.923	0.602
1271	1-20	0.881	0.514
1272	1-20	0.881	0.514
1273	1-21	0.839	0.518
1274	1-33	0.955	0.547
1275	1-26	0.884	0.488
1276	1-27	0.867	0.555
1277	1-18	0.822	0.521
1278	1-20	0.814	0.562
1279	1-24	0.921	0.756
1280	1-50	0.845	0.490
1332	1-27	0.968	0.912
1335	1-38	0.937	0.565
1338	1-23	0.993	0.924
1339	1-28	0.995	0.945
1340	1-28	0.995	0.945
1345	1-73	0.997	0.744
1346	1-24	0.985	0.690
1347	1-16	0.983	0.952
1348	1-16	0.949	0.869
1349	1-16	0.996	0.959
1354	1-49	0.989	0.784
1355	1-77	0.963	0.578
1356	1-24	0.974	0.882
1357	1-38	0.979	0.810
1359	1-24	0.981	0.938
1361	1-24	0.998	0.972
1362	1-22	0.963	0.884
1364	1-33	0.997	0.864
1366	1-20	0.890	0.648
1367	1-23	0.996	0.932
1370	1-38	0.983	0.894
1371	1-19	0.960	0.521
1372	1-18	0.986	0.589
1373	1-20	0.929	0.768
1375	1-17	0.977	0.921
1377	1-19	0.985	0.935
1379	1-40	0.961	0.521
1382	1-21	0.985	0.922
1384	1-51	0.976	0.781
1385	1-29	0.984	0.954
1386	1-19	0.981	0.939
1387	1-17	0.979	0.938
1388	1-33	0.953	0.828
1390	1-42	0.974	0.616
1394	1-28	0.989	0.912
1396	1-33	0.979	0.698
1397	1-24	0.927	0.726
1399	1-46	0.991	0.727

Table 6
1110

SEQ ID	Position	Maximum score	Average score
1400	1-44	0.900	0.657
1401	1-17	0.996	0.872
1402	1-39	0.989	0.941
1403	1-21	0.975	0.604
1404	1-16	0.957	0.870
1405	1-20	0.990	0.875
1407	1-71	0.981	0.566
1408	1-18	0.985	0.928
1410	1-14	0.941	0.861
1412	1-32	0.935	0.549
1419	1-20	0.989	0.960
1420	1-50	0.987	0.583
1421	1-27	0.977	0.849
1422	1-45	0.981	0.817
1423	1-28	0.988	0.923
1430	1-73	0.997	0.731
1432	1-23	0.992	0.956
1433	1-23	0.992	0.956
1437	1-60	0.976	0.737
1442	1-27	0.975	0.937
1467	1-57	0.931	0.514
1468	1-15	0.810	0.544
1469	1-41	0.926	0.451
1470	1-31	0.914	0.618
1471	1-33	0.889	0.542
1472	1-20	0.941	0.754
1473	1-55	0.929	0.541
1474	1-36	0.951	0.625
1475	1-18	0.897	0.608
1476	1-22	0.980	0.917
1477	1-73	0.959	0.450
1478	1-18	0.946	0.791
1479	1-22	0.951	0.739
1480	1-73	0.968	0.456
1481	1-25	0.879	0.674
1482	1-20	0.946	0.806
1483	1-24	0.992	0.825
1484	1-17	0.836	0.620
1485	1-53	0.917	0.508
1486	1-19	0.872	0.724
1487	1-58	0.954	0.452
1488	1-19	0.966	0.927
1489	1-36	0.979	0.862
1490	1-25	0.976	0.803
1491	1-26	0.898	0.658
1492	1-22	0.948	0.844
1493	1-22	0.894	0.673
1494	1-52	0.937	0.660
1495	1-37	0.930	0.614
1496	1-25	0.979	0.914
1497	1-22	0.972	0.929
1498	1-21	0.978	0.816
1499	1-24	0.839	0.692
1500	1-15	0.823	0.560
1501	1-16	0.960	0.845

Table 6

1111

SEQ ID	Position	Maximum score	Average score
1502	1-29	0.940	0.683
1503	1-12	0.832	0.523
1504	1-36	0.945	0.749
1505	1-33	0.843	0.488
1506	1-23	0.901	0.626
1507	1-20	0.834	0.505
1508	1-25	0.919	0.690
1509	1-44	0.885	0.513
1510	1-23	0.974	0.825
1511	1-13	0.941	0.847
1512	1-42	0.885	0.513
1513	1-18	0.903	0.592
1514	1-30	0.948	0.816
1515	1-16	0.944	0.818
1516	1-23	0.849	0.631
1517	1-13	0.813	0.610
1518	1-20	0.962	0.921
1519	1-23	0.823	0.495
1520	1-2	0.893	0.458
1521	1-17	0.902	0.762
1522	1-20	0.952	0.772
1523	1-23	0.991	0.925
1524	1-15	0.858	0.647
1525	1-15	0.979	0.961
1526	1-23	0.926	0.669
1527	1-23	0.942	0.686
1528	1-22	0.967	0.923
1529	1-22	0.913	0.519
1530	1-27	0.867	0.508
1531	1-15	0.807	0.631
1532	1-39	0.907	0.475
1533	1-24	0.823	0.503
1534	1-16	0.892	0.668
1535	1-16	0.860	0.607
1536	1-28	0.920	0.686
1537	1-20	0.801	0.618
1538	1-28	0.887	0.643
1539	1-21	0.927	0.568
1540	1-22	0.997	0.951
1541	1-22	0.985	0.827
1542	1-24	0.962	0.871
1543	1-22	0.972	0.932
1544	1-23	0.908	0.678
1545	1-27	0.899	0.579
1546	1-16	0.988	0.955
1547	1-16	0.873	0.622
1548	1-28	0.840	0.493
1549	1-15	0.889	0.689
1550	1-21	0.889	0.633
1551	1-44	0.981	0.617
1552	1-18	0.881	0.649
1553	1-16	0.805	0.631
1554	1-22	0.965	0.807
1555	1-26	0.928	0.744
1556	1-37	0.934	0.475

Table 6
1112

SEQ ID	Position	Maximum score	Average score
1557	1-31	0.935	0.631
1558	1-20	0.990	0.868
1559	1-13	0.853	0.530
1560	1-21	0.833	0.604
1561	1-25	0.922	0.642
1562	1-24	0.960	0.683
1563	1-31	0.908	0.677
1564	1-22	0.980	0.937
1565	1-17	0.857	0.523
1566	1-15	0.878	0.521
1567	1-19	0.861	0.660
1568	1-18	0.963	0.812
1569	1-32	0.965	0.659
1570	1-21	0.919	0.457
1571	1-33	0.931	0.799
1572	1-11	0.962	0.656
1573	1-22	0.969	0.862
1574	1-18	0.907	0.508
1575	1-19	0.952	0.751
1576	1-16	0.949	0.807
1577	1-20	0.984	0.912
1578	1-47	0.956	0.583
1579	1-30	0.965	0.639
1580	1-33	0.921	0.650
1581	1-21	0.996	0.915
1582	1-18	0.992	0.969
1583	1-19	0.820	0.492
1584	1-33	0.895	0.469
1585	1-37	0.987	0.701
1586	1-19	0.882	0.606
1587	1-19	0.896	0.652
1588	1-11	0.896	0.803
1589	1-22	0.977	0.769
1590	1-21	0.916	0.742
1591	1-15	0.909	0.760
1592	1-13	0.925	0.649
1593	1-26	0.963	0.782
1594	1-13	0.840	0.530
1595	1-35	0.984	0.835
1596	1-17	0.813	0.642
1597	1-20	0.822	0.535
1598	1-22	0.996	0.965
1599	1-17	0.866	0.603
1600	1-28	0.983	0.873
1601	1-36	0.963	0.813
1602	1-16	0.942	0.750
1603	1-16	0.827	0.545
1604	1-19	0.990	0.935
1605	1-28	0.910	0.588
1606	1-28	0.990	0.772
1607	1-30	0.944	0.835
1608	1-36	0.963	0.842
1609	1-18	0.937	0.839
1610	1-25	0.966	0.910
1611	1-33	0.963	0.577

Table 6

1113

SEQ ID	Position	Maximum score	Average score
1612	1-27	0.985	0.755
1613	1-20	0.970	0.737
1614	1-11	0.872	0.706
1615	1-19	0.932	0.541
1616	1-14	0.987	0.968
1617	1-52	0.948	0.570
1618	1-31	0.842	0.473
1619	1-27	0.985	0.927
1620	1-17	0.822	0.503
1621	1-61	0.982	0.770
1622	1-20	0.876	0.549
1623	1-19	0.872	0.552
1624	1-16	0.928	0.878
1625	1-20	0.914	0.495
1626	1-17	0.874	0.653
1627	1-16	0.969	0.917
1628	1-21	0.886	0.568
1629	1-45	0.931	0.487
1630	1-25	0.937	0.771
1631	1-23	0.811	0.514
1632	1-21	0.923	0.724
1633	1-17	0.833	0.543
1634	1-24	0.979	0.927
1635	1-20	0.972	0.802
1636	1-22	0.932	0.577
1637	1-18	0.894	0.643
1638	1-29	0.952	0.789
1639	1-38	0.918	0.617
1640	1-26	0.848	0.707
1641	1-23	0.989	0.864
1642	1-67	0.995	0.642
1643	1-18	0.970	0.681
1644	1-16	0.982	0.941
1645	1-24	0.971	0.908
1646	1-25	0.969	0.794
1647	1-40	0.863	0.548
1648	1-20	0.984	0.822
1649	1-15	0.803	0.568
1650	1-57	0.986	0.558
1651	1-26	0.975	0.763
1652	1-19	0.996	0.953
1653	1-34	0.994	0.961
1654	1-37	0.973	0.869
1655	1-21	0.901	0.716
1656	1-21	0.990	0.932
1657	1-42	0.959	0.693
1658	1-18	0.928	0.723
1659	1-16	0.914	0.756
1660	1-16	0.841	0.615
1661	1-70	0.932	0.496
1662	1-25	0.835	0.567
1663	1-39	0.958	0.854
1664	1-19	0.977	0.790
1665	1-19	0.962	0.794
1666	1-22	0.991	0.954

Table 6
1114

SEQ ID	Position	Maximum score	Average score
1667	1-39	0.842	0.525
1668	1-24	0.907	0.722
1669	1-52	0.950	0.667
1670	1-17	0.940	0.583
1671	1-26	0.926	0.642
1672	1-20	0.964	0.902
1673	1-22	0.947	0.788
1674	1-27	0.889	0.642
1675	1-16	0.985	0.900
1676	1-42	0.869	0.503
1677	1-73	0.976	0.512
1678	1-21	0.951	0.816
1679	1-25	0.946	0.771
1680	1-18	0.975	0.954
1681	1-19	0.926	0.729
1682	1-16	0.975	0.891
1683	1-25	0.967	0.881
1684	1-30	0.877	0.492
1685	1-23	0.990	0.905
1686	1-16	0.985	0.964
1687	1-20	0.969	0.803
1688	1-23	0.965	0.829
1689	1-20	0.894	0.502
1690	1-23	0.884	0.582
1691	1-19	0.972	0.705
1692	1-16	0.887	0.670
1693	1-21	0.961	0.741
1694	1-16	0.913	0.452
1695	1-25	0.946	0.829
1696	1-44	0.985	0.510
1697	1-32	0.920	0.468
1698	1-38	0.886	0.519
1699	1-15	0.978	0.904
1700	1-20	0.930	0.666
1701	1-25	0.988	0.903
1702	1-26	0.901	0.507
1703	1-38	0.971	0.793
1704	1-20	0.977	0.888
1705	1-30	0.822	0.550
1706	1-22	0.844	0.472
1707	1-16	0.923	0.641
1708	1-21	0.906	0.624
1709	1-22	0.977	0.880
1710	1-19	0.946	0.798
1711	1-24	0.928	0.557
1712	1-27	0.969	0.901
1713	1-30	0.926	0.755
1714	1-20	0.975	0.913
1715	1-23	0.927	0.606
1716	1-18	0.924	0.715
1717	1-31	0.826	0.618
1718	1-33	0.977	0.811
1719	1-26	0.934	0.636
1720	1-38	0.960	0.483
1721	1-36	0.962	0.537

Table 6
1115

SEQ ID	Position	Maximum score	Average score
1722	1-70	0.993	0.825
1723	1-33	0.928	0.642
1724	1-38	0.967	0.807
1725	1-18	0.988	0.897
1726	1-16	0.974	0.949
1727	1-42	0.951	0.468
1728	1-29	0.904	0.595
1729	1-41	0.938	0.600
1730	1-22	0.829	0.545
1731	1-52	0.990	0.466
1732	1-26	0.970	0.909
1733	1-24	0.971	0.865
1734	1-39	0.996	0.867
1735	1-45	0.961	0.593
1736	1-22	0.991	0.950
1737	1-25	0.978	0.623
1738	1-18	0.991	0.947
1739	1-47	0.926	0.486
1740	1-20	0.985	0.959
1741	1-32	0.995	0.972
1742	1-17	0.958	0.656
1743	1-62	0.964	0.638
1744	1-18	0.892	0.717
1745	1-27	0.992	0.934
1746	1-21	0.989	0.962
1747	1-67	0.991	0.685
1748	1-22	0.898	0.623
1749	1-15	0.981	0.945
1750	1-19	0.971	0.786
1751	1-36	0.983	0.664
1752	1-30	0.988	0.830
1753	1-28	0.953	0.866
1754	1-64	0.967	0.707
1755	1-56	0.967	0.554
1756	1-35	0.945	0.589
1757	1-19	0.922	0.737
1758	1-30	0.990	0.739
1759	1-25	0.951	0.864
1760	1-55	0.990	0.483
1761	1-29	0.982	0.792
1762	1-27	0.936	0.759
1763	1-29	0.960	0.805
1764	1-18	0.978	0.906
1765	1-22	0.962	0.920
1766	1-21	0.997	0.955
1767	1-25	0.942	0.847
1768	1-32	0.989	0.830
1769	1-25	0.880	0.630
1770	1-26	0.872	0.514
1771	1-29	0.990	0.648
1772	1-38	0.901	0.670
1773	1-25	0.992	0.955
1774	1-22	0.839	0.574
1775	1-33	0.970	0.887
1776	1-43	0.987	0.716

Table 6
1116

SEQ ID	Position	Maximum score	Average score
1777	1-29	0.831	0.548
1778	1-42	0.992	0.654
1779	1-20	0.936	0.580
1780	1-24	0.985	0.941
1781	1-48	0.996	0.882
1782	1-58	0.973	0.595
1783	1-22	0.899	0.602
1784	1-46	0.958	0.672
1785	1-10	0.881	0.707
1786	1-22	0.818	0.577
1787	1-53	0.903	0.465
1788	1-77	0.976	0.483
1789	1-72	0.973	0.475
1790	1-79	0.972	0.734
1791	1-71	0.958	0.519
1792	1-25	0.996	0.966
1793	1-75	0.975	0.571
1794	1-43	0.853	0.587
1795	1-17	0.948	0.513
1796	1-26	0.981	0.938
1797	1-33	0.986	0.753
1798	1-21	0.866	0.619
1799	1-31	0.965	0.885
1800	1-51	0.989	0.477
1801	1-65	0.977	0.706
1802	1-21	0.994	0.891
1803	1-24	0.986	0.956
1804	1-25	0.880	0.602
1805	1-24	0.991	0.954
1806	1-24	0.914	0.580
1807	1-71	0.956	0.528
1808	1-38	0.901	0.670
1809	1-43	0.975	0.765
1810	1-14	0.814	0.590
1811	1-14	0.909	0.490
1812	1-54	0.990	0.503
1813	1-76	0.999	0.992
1814	1-61	0.912	0.473
1815	1-20	0.975	0.944
1816	1-45	0.983	0.465
1817	1-24	0.936	0.769
1818	1-62	0.997	0.748
1819	1-74	0.986	0.539
1820	1-59	0.959	0.559
1821	1-22	0.860	0.539
1822	1-30	0.996	0.822

Table 7
1117

SEQ ID	Chromsomal location
1	13q12-q14
2	9q33-q34
3	2
4	13q12-q14
5	13q12-q14
6	13q12-q14
7	13q12-q14
8	13q12-q14
9	13q12-q14
10	17q11.2
11	19q13.3-q13.4
12	2
13	13q12-q14
14	8q
15	8q
16	11q13.1-q13.3
17	20q12
18	20q12
19	20q12
20	4
21	4
22	9q33-q34
23	9q33-q34
24	9q33-q34
25	9q33-q34
26	9q33-q34
27	9q33-q34
28	9q33-q34
29	9q33-q34
30	9q33-q34
31	9q33-q34
32	2
33	2
34	13q12-q14
35	13q12-q14
36	13q12-q14
37	13q12-q14
38	13q12-q14
39	13q12-q14
40	13q12-q14
41	13q12-q14
42	13q12-q14
43	13q12-q14
44	13q12-q14
45	13q12-q14
46	13q12-q14
47	13q12-q14
48	13q12-q14
49	13q12-q14
50	13q12-q14
51	13q12-q14
52	13q12-q14
53	13q12-q14
54	13q12-q14
55	13q12-q14

Table 7
1118

SEQ ID	Chromsomal location
56	13q12-q14
57	13q12-q14
58	13q12-q14
59	13q12-q14
60	13q12-q14
61	13q12-q14
62	13q12-q14
63	13q12-q14
64	13q12-q14
65	13q12-q14
66	13q12-q14
67	13q12-q14
68	13q12-q14
69	13q12-q14
70	13q12-q14
71	13q12-q14
72	13q12-q14
73	13q12-q14
74	13q12-q14
75	13q12-q14
76	13q12-q14
77	2
78	7
79	2
80	2
81	19q13.3-q13.4
82	19q13.3-q13.4
83	19q13.3-q13.4
84	19q13.3-q13.4
85	19q13.3-q13.4
86	19q13.3-q13.4
87	19q13.3-q13.4
88	19q13.3-q13.4
89	19q13.3-q13.4
90	19q13.3-q13.4
91	9q33-q34
92	13q12-q14
93	20q12
94	7
95	4
96	4
97	4
98	9q33-q34
99	9q33-q34
100	9q33-q34
101	9q33-q34
102	9q33-q34
103	9q33-q34
104	9q33-q34
105	2
106	13q12-q14
107	13q12-q14
108	13q12-q14
109	13q12-q14
110	13q12-q14

Table 7
1119

SEQ ID	Chromsomal location
111	13q12-q14
112	13q12-q14
113	13q12-q14
114	13q12-q14
115	13q12-q14
116	13q12-q14
117	13q12-q14
118	13q12-q14
119	13q12-q14
120	2
121	2
122	2
123	19q13.3-q13.4
124	19q13.3-q13.4
125	19q13.3-q13.4
126	13q12-q14
127	13q12-q14
128	20q12
129	4
130	4
131	9q33-q34
132	2
133	2
134	2
135	13q12-q14
136	13q12-q14
137	13q12-q14
138	13q12-q14
139	13q12-q14
140	17
141	6p21.3
142	13q12-q14
143	13q12-q14
144	13q12-q14
145	13q12-q14
146	13q12-q14
147	13q12-q14
148	13q12-q14
149	13q12-q14
150	13q12-q14
151	13q12-q14
152	13q12-q14
153	13q12-q14
154	13q12-q14
155	13q12-q14
156	2
157	2
158	19q13.3-q13.4
159	19q13.3-q13.4
160	19q13.3-q13.4
161	19q13.3-q13.4
162	4
163	4
164	9q33-q34
165	13q12-q14

Table 7
1120

SEQ ID	Chromsomal location
166	13q12-q14
167	13q12-q14
168	13q12-q14
169	22q12.1-12.3
170	13q12-q14
171	13q12-q14
172	13q12-q14
173	13q12-q14
174	13q12-q14
175	13q12-q14
176	8q
177	20q12
178	20q12
179	4
180	4
181	4
182	9q33-q34
183	9q33-q34
184	9q33-q34
185	3
186	9q33-q34
187	9q33-q34
188	9q33-q34
189	9q33-q34
190	9q33-q34
191	9q33-q34
192	9q33-q34
193	2
194	2
195	13q12-q14
196	13q12-q14
197	13q12-q14
198	13q12-q14
199	13q12-q14
200	13q12-q14
201	13q12-q14
202	13q12-q14
203	13q12-q14
204	13q12-q14
205	13q12-q14
206	13q12-q14
207	13q12-q14
208	13q12-q14
209	13q12-q14
210	13q12-q14
211	13q12-q14
212	13q12-q14
213	13q12-q14
214	19q13
215	13q12-q14
216	13q12-q14
217	13q12-q14
218	13q12-q14
219	13q12-q14
220	13q12-q14

Table 7
1121

SEQ ID	Chromsomal location
221	13q12-q14
222	13q12-q14
223	13q12-q14
224	13q12-q14
225	13q12-q14
226	13q12-q14
227	13q12-q14
228	13q12-q14
229	13q12-q14
230	13q12-q14
231	13q12-q14
232	13q12-q14
233	13q12-q14
234	13q12-q14
235	13q12-q14
236	13q12-q14
237	13q12-q14
238	5
239	5
240	19q13.3-q13.4
241	19q13.3-q13.4
242	19q13.3-q13.4
243	19q13.3-q13.4
244	19q13.3-q13.4
245	19q13.3-q13.4
246	19q13.3-q13.4
247	19q13.3-q13.4
248	19q13.3-q13.4
250	6
256	1p32
259	11q12-q13.1
268	18p11.22-p11.21
269	7q11.23
270	3
272	9q34.3
278	9q32-q33
279	14q11.2
280	14q11.2
283	2
285	13
298	20q12-q13.1
303	1
305	19
306	19
310	4p16-p15
311	6
316	3p22-p21.3
326	1p31.1-p22.3
335	11pter-p15.5
336	3
350	11q
353	3
355	8p21-p12
356	1q23-q25.1
357	1q23-q25.1

Table 7
1122

SEQ ID	Chromsomal location
359	20q13.2-q13.33
360	13
361	13
362	22q13.1
369	6
373	2p24.3-p24.1
374	2p24.3-p24.1
383	11q13
384	19q13.2
388	17q11-q21.1
398	8p23.2-p23.1
403	19
407	11
421	19q13.1
427	20q12-q13.12
428	17
429	17
431	11q13
432	7q35
433	X
435	6q22.2-22.33
437	19
439	16q24.3
445	19q13
446	12
452	14
453	3
456	14
457	10
458	10
459	3p21.1-q13.13
460	1p36
470	14q31
475	4q11-q13
476	6
477	15q21-q22
478	15q24-q26
493	19
496	6q24.1-24.3
497	15
501	11q13
505	1q21
506	6p21.3
507	3
510	1q21.3
512	14
513	9
515	1
521	7q32-34
522	7q32-34
532	2
545	q21.2-21.3
547	11
551	11q22
556	10,

Table 7
1123

SEQ ID	Chromsomal location
557	9p24.1-24.3,
559	16
560	18
561	9
562	22q11.22-12.3.
565	6q22.3-23.3
566	6q22.1-22.33,
567	1
568	11
569	6q21
571	18,
572	15,
573	5
574	5
575	6p21.1-21.2.
576	8,
577	10
578	1
579	12
580	1
581	6q16.3-22.1,
582	3
583	10
585	3
587	1
588	5
590	4
592	1q24.
593	1
594	8
595	17,
596	11
597	5
598	16
599	11
600	13,
601	11q
603	2
604	6q25.2-26,
606	1
607	15
608	9
609	1q24
610	1
611	4
612	17,
613	8
614	17,
615	15
616	6,
617	15
618	2
619	3
620	17
621	8

Table 7
1124

SEQ ID	Chromsomal location
622	14
623	6q24.1-25.2,
624	2
625	9
626	8
627	12q24
629	20,
630	NA
631	2
632	2
633	Xp11.21-11.22
634	17
636	2
637	22
638	1
639	3
640	19,
641	1
642	7
643	5
645	17
647	1,
649	6
650	7
651	5
652	19,
653	20q11.1-11.23,
654	1
655	3
656	8
657	16
659	9
660	18
662	6p21.3,
665	X
666	5
667	1
669	2
670	13,
671	1
672	15
673	9,
674	10
675	9,
676	7
678	16
679	X
680	11,
681	19,
683	8
684	4
685	6q16.1-16.3,
686	10,
687	14
688	4

Table 7
1125

SEQ ID	Chromsomal location
689	6q26-27,
690	1p35.1-36.13,
692	6q26-27,
695	12
700	9,
701	5
702	2
703	8
704	10,
705	19
706	14
708	19,
709	17
711	16
712	16
713	5
714	16
715	19
716	16
717	12
718	15
719	15
720	14
721	16
722	5
723	6,
724	12q
725	1
726	8
727	15,
728	2
729	7
730	17,
731	21q22.1,
732	20p12
733	11
734	1
735	15
736	2
737	1p36.21-36.33.
738	1
739	6q21-22.31,
740	15
742	12
743	UL
744	13q33.3-34,
745	17,
746	12
747	2
749	16
752	17
754	16
755	20q12-13.12.
756	19
757	14

Table 7
1126

SEQ ID	Chromsomal location
758	8,
759	6,
760	22
761	19
763	13,
764	1q32.1-41
765	8,
767	20
769	11q,
770	1
771	6p22.3-24.1,
772	9p23-24.3,
773	17
774	19
775	3
776	3
777	22q12
779	1p36.13-36.31,
780	17
781	7
783	4
784	6,
785	1
786	21q22.1,
787	6
788	1
789	15
790	20,
791	9
793	10,
794	16
796	18
797	18
798	10
799	8,
800	16
801	UNK
803	9,
807	20q13.1.
808	10,
809	3
810	UNK
815	20.
818	1q25.1-31.1,
820	10
821	20p12.2-13,
822	20
823	4,
824	1
826	5
827	8
829	7
830	1p21.3-22.3,
832	1
833	12q

Table 7
1127

SEQ ID	Chromsomal location
834	6
836	6,
837	10
838	9p11.2-21,
839	11
840	5
841	17
842	11q
844	1
845	11q,
846	9
848	13,
849	12
852	1
853	16
854	15
856	6q25.3-26
857	6,
858	1
859	11
860	5p,
861	11
862	6,
864	1q22-q23,
865	12p
866	1q32.2-41
867	2
868	13q33.1-34,
869	6p21.3,
870	3
872	1
873	3
874	19,
876	9,
877	16p13
878	5
879	16
880	5
881	16
882	15
883	15
884	9
885	8p11.2,
886	17
887	5
888	6,
889	13,
890	11
891	11
892	Xq22.3-23,
894	9,
895	10
896	15
897	11
898	1,

Table 7
1128

SEQ ID	Chromsomal location
899	6q25.2-26,
900	12
901	1
902	19
903	19,
904	4
905	5
906	5
908	19
909	4,
910	19,
911	15

Table 8

1129

SEQ ID NO:	Number of Transmembrane Domains	For each Transmembrane Domain, its Transmembrane Domain Position in SEQ ID NO: and its TM Pred Score
1037	1	100-115:1952
1038	1	732-749:2593
1039	1	181-201:2410
1040	2	53-68:1828 132-149:2533
1041	2	53-69:2959 121-140:2878
1042	1	536-560:2906
1043	1	63-82:2545
1044	5	86-102:1766 189-205:2721 229-244:1878 273-300:1714 385-405:1946
1045	1	629-645:2430
1046	1	59-75:2149
1047	1	306-332:2773
1048	1	118-136:2329
1049	2	98-113:2861 220-243:2391
1050	1	151-169:2618
1051	2	94-110:2524 124-146:2138
1052	1	73-87:2180
1053	1	206-226:2584
1054	1	402-419:2096
1055	1	343-361:1953
1056	1	132-154:2199
1057	1	590-613:2402
1058	2	89-105:1748 155-173:2433
1059	1	201-222:2190
1060	4	254-277:2256 317-332:1771 442-460:2005 530-544:2110
1061	2	169-186:1866 239-259:2042
1062	1	63-77:1794
1063	1	227-248:3456
1064	1	133-148:2558
1065	3	435-453:1849 505-526:2495 697-712:2057
1066	1	317-340:2214
1067	1	173-192:2637
1068	1	63-79:1933
1069	1	124-146:3384
1070	3	82-102:2213 115-135:1769 160-185:2317
1071	1	312-329:2354
1072	2	116-131:3056 188-209:2254
1073	6	48-71:1708 174-196:2300 237-254:1918 359-378:1887 413-435:1864 501-518:2625
1074	6	136-159:1708 262-284:2300 325-342:1918 447-466:1887 501-523:1864 589-606:2625
1075	1	352-376:2946
1076	3	106-125:2854 226-241:1973 277-300:2759
1077	4	85-105:2047 208-225:1907 309-330:2122 454-471:2461
1079	1	60-75:2189
1081	3	192-214:1705 236-259:1933 436-453:2349
1082	1	459-477:1896
1083	1	144-159:3028
1084	1	144-159:3028
1085	1	436-455:2525
1086	1	705-724:2525
1093	2	93-108:2014 249-264:2324
1094	5	145-165:2633 316-331:2180 399-412:1770 481-496:2328 541-560:2589

Table 8

1130

SEQ ID NO:	Number of Transmembrane Domains	For each Transmembrane Domain, its Transmembrane Domain Position in SEQ ID NO: and its TM Pred Score
1095	1	73-92:1951
1097	1	85-103:2195
1099	1	160-176:2085
1100	1	256-272:2085
1101	1	210-226:2085
1102	1	63-94:3259
1103	2	184-201:2183 245-262:1812
1104	1	276-295:3080
1106	1	179-194:2620
1110	1	111-129:2519
1112	1	169-190:2680
1113	3	61-82:2141 99-134:1715 119-139:2765
1114	1	65-85:1713
1115	3	123-137:2644 190-218:2074 300-314:2588
1116	2	98-123:2354 270-295:2148
1117	1	77-92:1791
1118	1	68-88:2672
1119	1	1524-1547:2939
1121	1	95-113:2958
1123	2	92-107:1923 162-178:2760
1124	1	71-94:1835
1125	1	379-403:3221
1127	1	152-182:1795
1129	3	201-217:2437 338-353:1761 449-466:2589
1130	2	99-114:1754 108-130:2731
1131	1	1177-1193:3038
1132	1	95-111:2301
1133	2	205-227:1715 307-322:1735
1134	1	308-330:2431
1136	5	92-107:1734 298-311:2063 363-378:1720 382-399:1988 453-471:2040
1137	2	56-75:2481 127-148:2269
1138	1	228-251:1822
1139	4	97-115:1903 177-194:1919 889-905:2063 988-1008:2027
1141	1	223-242:2971
1143	3	63-86:2169 177-194:1878 271-288:2186
1144	2	116-136:2390 179-194:2530
1146	2	66-82:2701 110-126:1755
1147	2	74-106:2580 139-156:1958
1148	1	522-544:2644
1149	2	83-97:2024 200-216:2275
1150	1	200-216:2275
1151	1	92-109:2588
1152	2	145-169:1834 317-346:1891
1155	4	64-83:2948 218-232:2016 452-480:1829 535-553:1999
1156	1	311-330:2524
1157	1	78-111:2597
1159	1	163-180:2270
1330	1	264-282:2674
1331	1	105-128:2620
1332	1	141-164:3091
1333	1	394-409:1914
1334	1	390-410:1947
1335	1	67-82:1917

Table 8

1131

SEQ ID NO:	Number of Transmembrane Domains	For each Transmembrane Domain, its Transmembrane Domain Position in SEQ ID NO: and its TM Pred Score
1336	1	301-317:3356
1337	1	301-317:3356
1338	1	427-443:1894
1339	2	103-119:2524 133-155:2138
1340	2	94-110:2524 124-146:2138
1341	2	61-78:1768 212-233:2126
1342	1	139-160:2023
1343	1	331-353:1902
1344	1	99-117:2054
1345	1	52-67:1997
1346	1	67-80:2411
1347	1	367-384:2888
1348	1	457-476:2898
1349	2	202-217:1923 272-288:2760
1350	5	266-284:2563 328-346:2525 390-408:2516 452-470:2456 514-532:2395
1351	1	94-116:2763
1352	2	45-62:2164 71-85:1838
1353	1	482-504:3155
1354	3	1-17:2284 75-90:1824 145-160:2079
1355	1	12-28:1796
1356	1	332-356:3221
1357	1	9-30:2498
1358	3	202-215:2016 256-281:1796 283-312:1900
1359	1	267-284:3050
1360	3	229-245:2437 316-333:1885 429-446:2589
1361	1	1-17:2914
1362	1	4-21:2014
1363	1	962-980:1762
1364	1	12-31:2460
1365	1	38-54:3201
1366	1	103-119:2300
1367	1	1-15:2225
1368	1	48-64:1711
1369	1	48-64:1711
1370	1	21-36:2592
1371	2	290-307:2420 419-433:2394
1372	1	66-81:2345
1373	1	3-18:1914
1374	1	110-124:2032
1375	1	3-18:1862
1376	4	37-56:2540 102-127:1708 194-209:2784 434-453:2036
1377	1	1-20:2264
1378	3	259-274:2102 330-358:2448 416-434:2702
1379	1	24-43:2348
1380	1	196-211:1704
1381	3	159-176:1865 238-260:2690 305-319:2565
1382	1	262-288:2789
1383	2	60-89:2283 119-140:1980
1384	1	21-41:2833
1385	1	227-248:3456
1386	1	3-19:2081
1387	1	162-180:3181
1388	1	12-27:2098

Table 8

1132

SEQ ID NO:	Number of Transmembrane Domains	For each Transmembrane Domain, its Transmembrane Domain Position in SEQ ID NO: and its TM Pred Score
1389	1	487-503:2039
1390	2	95-111:2234 155-173:2180
1391	2	87-106:2547 186-206:1903
1392	3	142-162:2149 169-184:1733 265-283:2036
1393	3	83-110:1977 142-159:1729 238-254:2361
1394	1	12-30:2458
1395	1	61-76:2746
1396	1	14-31:1963
1397	1	1060-1079:2742
1398	1	220-244:2016
1399	1	17-36:2664
1400	1	21-41:1851
1401	1	37-69:2282
1402	1	24-60:1926
1403	1	55-75:2438
1404	1	237-252:2493
1405	1	1-20:1866
1406	1	172-190:1781
1407	1	90-111:2881
1408	1	6-23:2294
1409	1	477-499:2659
1410	1	231-249:2797
1411	3	64-84:1993 95-110:1932 149-167:2173
1412	3	166-182:1937 216-239:1819 326-341:1779
1413	1	154-169:2224
1414	1	241-254:1760
1415	2	71-97:1818 234-254:2475
1416	1	143-164:2551
1417	2	104-122:1815 147-162:2031
1418	2	121-135:2273 209-234:2186
1419	2	8-27:2032 82-102:1765
1420	1	26-47:2557
1421	3	18-34:1798 220-243:1742 301-318:1915
1422	1	27-42:3053
1423	1	6-21:1974
1424	1	345-360:2050
1425	1	44-65:2195
1426	1	763-779:1916
1427	1	448-469:2686
1428	1	597-614:2205
1429	1	194-210:2157
1430	2	22-44:2983 52-67:1999
1431	2	22-39:1830 91-106:2145
1432	1	6-26:2422
1433	1	6-26:2422
1434	1	72-89:1942
1435	2	128-146:1770 337-352:3007
1436	1	88-105:1803
1437	1	1013-1035:2346
1438	4	574-589:1938 650-668:2275 720-735:1944 793-810:1729
1439	4	655-670:1938 731-749:2275 801-816:1944 874-891:1729
1440	1	65-81:2339
1441	1	131-151:1772
1442	2	5-22:1872 248-273:2467

Table 8
1133

SEQ ID NO:	Number of Transmembrane Domains	For each Transmembrane Domain, its Transmembrane Domain Position in SEQ ID NO: and its TM Pred Score
1443	3	179-194:2318 387-403:3014 442-465:1871
1444	2	58-74:2684 238-264:2576
1720	1	89-107:1832
1721	1	225-240:2165
1722	2	13-29:2422 49-63:2158
1723	1	129-144:1704
1724	1	12-28:1900
1725	4	1-22:1840 143-158:1938 181-198:2860 247-265:2284
1726	1	1-15:1790
1727	2	100-122:2447 199-217:2147
1728	1	12-28:1802
1729	1	21-37:1706
1730	1	328-343:2384
1731	3	33-60:2908 185-211:2596 237-258:1818
1732	1	279-309:1795
1733	1	6-26:2040
1734	1	14-34:1939
1735	1	17-38:1933
1736	2	10-25:2484 95-110:1787
1737	2	5-21:1862 109-125:2714
1738	1	1-21:1881
1739	1	393-414:2402
1740	1	3-21:2189
1741	3	15-33:3158 109-123:2786 364-380:2232
1742	1	564-580:1725
1743	2	40-60:2740 169-189:3006
1744	1	214-228:2582
1745	1	3-19:2099
1746	2	4-22:2753 247-263:2558
1747	1	43-60:2160
1748	1	195-217:2199
1749	4	304-319:1707 427-447:1983 547-562:2389 657-683:2065
1750	5	2-17:2136 753-768:2335 810-831:1715 906-928:1710 1009-1031:2357
1751	1	337-352:2864
1752	1	1-24:3347
1753	1	621-644:2150
1754	1	88-106:2133
1755	4	67-89:2584 130-148:1837 239-261:1922 334-349:2621
1756	1	20-35:1702
1757	1	471-488:1852
1758	2	8-25:2374 247-265:1721
1759	1	10-26:2268
1760	2	37-55:2350 79-102:1867
1761	1	3-16:1751
1762	4	10-29:2708 158-183:2332 413-430:1706 514-532:2104
1763	1	531-558:2381
1764	1	1-15:2095
1765	1	3-20:1765
1766	1	3-27:2376
1767	1	11-39:1868
1768	1	150-169:1896
1769	1	91-112:2655
1770	1	347-362:1792

Table 8
1134

SEQ ID NO:	Number of Transmembrane Domains	For each Transmembrane Domain, its Transmembrane Domain Position in SEQ ID NO: and its TM Pred Score
1771	1	717-737:3080
1772	1	9-24:1787
1773	2	1-16:1977 85-110:2971
1774	3	492-510:2266 517-532:1752 675-696:1808
1775	3	16-33:2461 94-113:2485 221-247:2232
1776	1	24-39:2149
1777	1	108-123:2281
1778	2	23-42:3401 179-201:3489
1779	1	296-311:1881
1780	1	280-303:2645
1781	1	22-37:2170
1782	1	313-332:1963
1783	7	243-261:2338 288-311:1992 401-429:1705 502-519:1819 556-568:1888 597-614:1780 675-690:2102
1784	1	1433-1457:3108
1785	1	390-403:1855
1786	2	103-122:1737 738-756:2220
1787	2	116-131:2359 173-193:1746
1788	1	128-144:2443
1789	1	73-97:1982
1790	1	103-124:2547
1791	1	53-69:2536
1792	3	84-99:2680 1083-1098:1729 1147-1167:2267
1793	1	59-74:2644
1794	2	24-39:2073 69-92:1922
1795	1	59-78:2490
1796	2	1101-1121:2566 1224-1244:2000
1797	3	54-73:1789 113-131:1860 182-195:2408
1798	2	76-92:1943 135-155:3247
1799	1	141-159:3106
1800	1	248-266:1883
1801	2	413-430:1851 496-521:2037
1802	1	782-811:1739
1803	3	85-108:1832 117-138:1746 166-187:2659
1804	1	183-200:1880
1805	1	549-568:1822
1806	2	121-142:2091 191-210:2580
1807	3	52-67:2292 112-127:1756 215-232:2516
1808	1	99-115:1824
1809	1	24-41:1826
1810	3	710-738:2388 769-792:1779 797-815:1896
1811	1	71-93:2069
1812	1	97-117:1891
1813	3	12-27:2868 38-54:1801 59-89:3042
1814	1	404-422:2347
1815	1	1-19:2068
1816	2	62-84:2012 118-134:1970
1817	1	68-83:2632
1818	2	3-22:2491 47-61:1754
1819	1	1187-1209:3678
1820	6	4-29:1727 87-110:3204 95-129:1851 165-190:2822 214-230:1867 245-261:1911
1821	1	324-342:2300
1822	1	4-24:1911

Table 9
1135

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
1	912	1823	2479	784_2167
2	913	1824	2480	790_12732
3	914	1825	2481	787_7952
4	915	1826	2482	787_7952
5	916			
6	917	1827	2483	787_5660
7	918	1828	2484	790_6350
8	919	1829	2485	790_18138
9	920	1830	2486	784_2658
10	921	1831	2487	788_11684
11	922			
12	923	1832	2488	789_1765
13	924	1833	2489	784_6512
14	925	1834	2490	789_4745
15	926	1835	2491	790_14655
16	927	1836	2492	791_2272
17	928	1837	2493	791_1348
18	929	1838	2494	790_23
19	930	1839	2495	784_5039
20	931	1840	2496	787_8518
21	932	1841	2497	784_5125
22	933			
23	934			
24	935	1842	2498	790_26893
25	936	1843	2499	785_3384
26	937	1844	2500	791_2238
27	938	1845	2501	784_7881
28	939			
29	940			
30	941	1846	2502	785_197
31	942	1847	2503	785_836
32	943	1848	2504	784_8990
33	944	1849	2505	792_6041
34	945	1850	2506	792_873
35	946			
36	947	1851	2507	784_4339
37	948			
38	949	1852	2508	792_5188
39	950			
40	951	1853	2509	784_6463
41	952	1854	2510	784_2235
42	953	1855	2511	784_2849
43	954	1856	2512	785_206
44	955	1857	2513	787_6368
45	956	1858	2514	788_5838
46	957	1859	2515	784_7012
47	958			
48	959	1860	2516	785_835
49	960	1861	2517	784_7305
50	961			
51	962	1862	2518	784_8815

Table 9
1136

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
52	963	1863	2519	784_7195
53	964	1864	2520	787_6723
54	965			
55	966	1865	2521	787_5698
56	967	1866	2522	790_12578
57	968	1867	2523	784_6485
58	969	1868	2524	784_1896
59	970	1869	2525	792_1194
60	971	1870	2526	784_9157
61	972			
62	973	1871	2527	784_1408
63	974	1872	2528	784_2508
64	975	1873	2529	784_1049
65	976			
66	977			
67	978			
68	979			
69	980			
70	981	1874	2530	787_6121
71	982	1875	2531	785_2903
72	983	1876	2532	787_10197
73	984			
74	985	1877	2533	787_10224
75	986	1878	2534	789_5808
76	987			
77	988	1879	2535	784_6287
78	989	1880	2536	785_582
79	990			
80	991			
81	992	1881	2537	790_12952
82	993			
83	994	1882	2538	790_13887
84	995	1883	2539	784_7925
85	996			
86	997			
87	998	1884	2540	790_11010
88	999	1885	2541	790_17371
89	1000			
90	1001			
91	1002	1886	2542	784_1560
92	1003	1887	2543	784_1260
93	1004	1888	2544	790_21336
94	1005	1889	2545	784_7912
95	1006			
96	1007	1890	2546	784_8528
97	1008	1891	2547	784_8105
98	1009	1892	2548	787_5314
99	1010	1893	2549	784_7469
100	1011	1894	2550	790_11802
101	1012	1895	2551	787_5599
102	1013	1896	2552	784_5534

Table 9
1137

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
103	1014			
104	1015	1897	2553	791_3043
105	1016	1898	2554	784_8916
106	1017	1899	2555	784_1271
107	1018			
108	1019			
109	1020	1900	2556	784_6527
110	1021			
111	1022	1901	2557	790_14183
112	1023	1902	2558	791_1570
113	1024	1903	2559	787_2154
114	1025	1904	2560	787_2849
115	1026			
116	1027			
117	1028			
118	1029	1905	2561	790_23824
119	1030	1906	2562	787_10284
120	1031	1907	2563	790_13062
121	1032			
122	1033			
123	1034			
124	1035	1908	2564	787_3576
125	1036			
126	1037			
127	1038	1909	2565	789_2490
128	1039	1910	2566	784_2340
129	1040	1911	2567	784_3449
130	1041	1912	2568	787_9834
131	1042	1913	2569	787_7563
132	1043			
133	1044	1914	2570	784_969
134	1045	1915	2571	784_9071
135	1046	1916	2572	785_1259
136	1047	1917	2573	790_19506
137	1048	1918	2574	784_3978
138	1049	1919	2575	784_3848
139	1050	1920	2576	789_6174
140	1051	1921	2577	785_1465
141	1052	1922	2578	787_7763
142	1053	1923	2579	790_25889
143	1054			
144	1055	1924	2580	784_4674
145	1056	1925	2581	787_8960
146	1057	1926	2582	787_2258
147	1058	1927	2583	787_2290
148	1059	1928	2584	784_8266
149	1060	1929	2585	784_1397
150	1061	1930	2586	784_8164
151	1062	1931	2587	785_1003
152	1063			
153	1064			

Table 9
1138

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
154	1065	1932	2588	784_2498
155	1066	1933	2589	787_5189
156	1067			
157	1068	1934	2590	787_10359
158	1069			
159	1070			
160	1071	1935	2591	790_17261
161	1072	1936	2592	784_9629
162	1073	1937	2593	784_3405
163	1074	1938	2594	784_3405
164	1075	1939	2595	790_4043
165	1076	1940	2596	787_3900
166	1077	1941	2597	787_9753
167	1078	1942	2598	787_4766
168	1079	1943	2599	789_3521
169	1080	1944	2600	784_8097
170	1081			
171	1082	1945	2601	784_735
172	1083	1946	2602	784_4418
173	1084	1947	2603	784_4418
174	1085			
175	1086			
176	1087	1948	2604	784_1006
177	1088	1949	2605	784_1528
178	1089			
179	1090			
180	1091	1950	2606	791_2053
181	1092			
182	1093	1951	2607	788_6860
183	1094	1952	2608	785_1010
184	1095	1953	2609	784_6854
185	1096	1954	2610	784_8679
186	1097	1955	2611	790_19249
187	1098	1956	2612	784_5566
188	1099	1957	2613	790_3027
189	1100	1958	2614	790_3027
190	1101	1959	2615	790_3027
191	1102			
192	1103	1960	2616	791_2652
193	1104	1961	2617	784_7116
194	1105	1962	2618	789_1658
195	1106	1963	2619	787_7673
196	1107	1964	2620	790_3240
197	1108			
198	1109	1965	2621	784_6361
199	1110	1966	2622	784_297
200	1111	1967	2623	790_13930
201	1112			
202	1113	1968	2624	784_8933
203	1114			
204	1115			

Table 9
1139

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
205	1116			
206	1117			
207	1118	1969	2625	784_7603
208	1119	1970	2626	787_5453
209	1120	1971	2627	789_6377
210	1121	1972	2628	784_7446
211	1122	1973	2629	784_5422
212	1123	1974	2630	784_2530
213	1124	1975	2631	787_7257
214	1125	1976	2632	784_5473
215	1126	1977	2633	784_1793
216	1127	1978	2634	784_10027
217	1128			
218	1129	1979	2635	787_2898
219	1130	1980	2636	788_9208
220	1131	1981	2637	787_2305
221	1132	1982	2638	784_8556
222	1133			
223	1134	1983	2639	787_5766
224	1135	1984	2640	790_4531
225	1136	1985	2641	784_6708
226	1137	1986	2642	790_19316
227	1138	1987	2643	784_1784
228	1139	1988	2644	784_1698
229	1140	1989	2645	787_1368
230	1141	1990	2646	789_6192
231	1142	1991	2647	784_4498
232	1143			
233	1144	1992	2648	789_6042
234	1145			
235	1146	1993	2649	790_4461
236	1147			
237	1148	1994	2650	784_2675
238	1149	1995	2651	789_4591
239	1150	1996	2652	789_4591
240	1151	1997	2653	790_13145
241	1152			
242	1153	1998	2654	791_4932
243	1154			
244	1155	1999	2655	784_10141
245	1156	2000	2656	784_10225
246	1157	2001	2657	784_7722
247	1158			
248	1159			
249	1160	2002	2658	787_3228
250	1161	2003	2659	785_3642
251	1162	2004	2660	784_6469
252	1163	2005	2661	787_6106
253	1164	2006	2662	791_2793
254	1165			
255	1166	2007	2663	784_3318

Table 9
1140

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
256	1167			
257	1168	2008	2664	789_6270
258	1169	2009	2665	788_13058
259	1170	2010	2666	787_5541
260	1171			
261	1172	2011	2667	784_7891
262	1173	2012	2668	784_4405
263	1174	2013	2669	784_7585
264	1175	2014	2670	784_7585
265	1176	2015	2671	785_3390
266	1177	2016	2672	789_6254
267	1178	2017	2673	785_3073
268	1179	2018	2674	790_16443
269	1180			
270	1181	2019	2675	790_21097
271	1182	2020	2676	787_8948
272	1183	2021	2677	784_8624
273	1184			
274	1185	2022	2678	785_2309
275	1186			
276	1187	2023	2679	784_1834
277	1188	2024	2680	787_8921
278	1189	2025	2681	784_7125
279	1190	2026	2682	785_2903
280	1191	2027	2683	785_2903
281	1192			
282	1193			
283	1194	2028	2684	791_2389
284	1195			
285	1196	2029	2685	784_7647
286	1197	2030	2686	784_3528
287	1198	2031	2687	784_5750
288	1199			
289	1200	2032	2688	789_3496
290	1201			
291	1202			
292	1203	2033	2689	790_16699
293	1204	2034	2690	785_3735
294	1205	2035	2691	788_12224
295	1206	2036	2692	787_6084
296	1207			
297	1208	2037	2693	784_330
298	1209	2038	2694	791_2972
299	1210	2039	2695	790_24002
300	1211			
301	1212	2040	2696	784_528
302	1213	2041	2697	787_1611
303	1214	2042	2698	785_1187
304	1215	2043	2699	784_8087
305	1216	2044	2700	789_4427
306	1217	2045	2701	789_4427

Table 9
1141

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
307	1218			
308	1219	2046	2702	785_2691
309	1220	2047	2703	785_1940
310	1221	2048	2704	784_5176
311	1222	2049	2705	784_1451
312	1223	2050	2706	789_5236
313	1224	2051	2707	787_5175
314	1225	2052	2708	784_8301
315	1226	2053	2709	785_3698
316	1227	2054	2710	785_2838
317	1228			
318	1229			
319	1230	2055	2711	784_10105
320	1231	2056	2712	784_4974
321	1232	2057	2713	785_3025
322	1233	2058	2714	785_3028
323	1234	2059	2715	785_3031
324	1235	2060	2716	785_2106
325	1236	2061	2717	785_3032
326	1237	2062	2718	792_7466
327	1238	2063	2719	785_2107
328	1239	2064	2720	785_3035
329	1240	2065	2721	785_3037
330	1241	2066	2722	785_3038
331	1242	2067	2723	785_3038
332	1243	2068	2724	785_2108
333	1244	2069	2725	785_3043
334	1245	2070	2726	785_3045
335	1246	2071	2727	785_2114
336	1247	2072	2728	785_483
337	1248	2073	2729	785_609
338	1249	2074	2730	785_1502
339	1250	2075	2731	785_2157
340	1251	2076	2732	785_3106
341	1252	2077	2733	785_3508
342	1253			
343	1254	2078	2734	785_3114
344	1255	2079	2735	785_3115
345	1256	2080	2736	785_2161
346	1257			
347	1258	2081	2737	785_3123
348	1259	2082	2738	785_854
349	1260	2083	2739	785_1504
350	1261	2084	2740	790_3585
351	1262			
352	1263	2085	2741	784_1062
353	1264	2086	2742	784_9616
354	1265			
355	1266	2087	2743	788_604
356	1267	2088	2744	784_9474
357	1268	2089	2745	784_9474

Table 9
1142

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
358	1269			
359	1270			
360	1271	2090	2746	788_6828
361	1272	2091	2747	788_6828
362	1273	2092	2748	784_8575
363	1274	2093	2749	790_21803
364	1275	2094	2750	784_5329
365	1276	2095	2751	784_10122
366	1277	2096	2752	784_3644
367	1278			
368	1279	2097	2753	787_2863
369	1280	2098	2754	784_854
370	1281			
371	1282			
372	1283	2099	2755	787_3968
373	1284	2100	2756	785_2864
374	1285	2101	2757	785_2864
375	1286			
376	1287	2102	2758	784_4739
377	1288			
378	1289	2103	2759	791_771
379	1290	2104	2760	792_4497
380	1291	2105	2761	784_4833
381	1292	2106	2762	785_3195
382	1293	2107	2763	784_6243
383	1294	2108	2764	784_1134
384	1295	2109	2765	784_10176
385	1296	2110	2766	784_3781
386	1297	2111	2767	785_2441
387	1298	2112	2768	787_4817
388	1299	2113	2769	784_3255
389	1300			
390	1301	2114	2770	784_9436
391	1302	2115	2771	784_5232
392	1303	2116	2772	784_4604
393	1304			
394	1305	2117	2773	784_7986
395	1306	2118	2774	787_10365
396	1307	2119	2775	784_4897
397	1308			
398	1309	2120	2776	787_5541
399	1310	2121	2777	787_7655
400	1311	2122	2778	784_1002
401	1312	2123	2779	787_8365
402	1313			
403	1314	2124	2780	784_9956
404	1315	2125	2781	787_7927
405	1316	2126	2782	787_10138
406	1317	2127	2783	787_5878
407	1318	2128	2784	784_6962
408	1319	2129	2785	784_1341

Table 9

1143

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No. SEQ ID NO.) *
409	1320	2130	2786	787_894
410	1321			
411	1322	2131	2787	784_5866
412	1323	2132	2788	784_5734
413	1324			
414	1325			
415	1326	2133	2789	788_11985
416	1327			
417	1328	2134	2790	791_1605
418	1329			
419	1330	2135	2791	784_3232
420	1331	2136	2792	784_1670
421	1332			
422	1333	2137	2793	784_2377
423	1334	2138	2794	788_2631
424	1335	2139	2795	784_8666
425	1336	2140	2796	785_1109
426	1337	2141	2797	785_1109
427	1338	2142	2798	784_6176
428	1339	2143	2799	785_1465
429	1340	2144	2800	785_1465
430	1341	2145	2801	784_5369
431	1342	2146	2802	787_8763
432	1343	2147	2803	784_5253
433	1344	2148	2804	789_2568
434	1345	2149	2805	790_3055
435	1346	2150	2806	790_10356
436	1347	2151	2807	785_2811
437	1348	2152	2808	784_2496
438	1349	2153	2809	784_2530
439	1350	2154	2810	784_2168
440	1351	2155	2811	784_7505
441	1352	2156	2812	784_6670
442	1353	2157	2813	787_2168
443	1354	2158	2814	784_3022
444	1355	2159	2815	790_1217
445	1356	2160	2816	784_5473
446	1357	2161	2817	784_7905
447	1358			
448	1359	2162	2818	784_9436
449	1360	2163	2819	787_2898
450	1361			
451	1362			
452	1363	2164	2820	784_4625
453	1364	2165	2821	785_2622
454	1365			
455	1366	2166	2822	787_2386
456	1367	2167	2823	788_9391
457	1368	2168	2824	784_10104
458	1369	2169	2825	784_10104
459	1370	2170	2826	787_10366

Table 9
1144

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No. SEQ ID NO.) *
460	1371	2171	2827	784_6453
461	1372	2172	2828	785_1337
462	1373	2173	2829	787_5778
463	1374	2174	2830	784_5025
464	1375			
465	1376	2175	2831	785_739
466	1377	2176	2832	787_1269
467	1378			
468	1379			
469	1380			
470	1381	2177	2833	785_326
471	1382	2178	2834	784_8341
472	1383	2179	2835	787_757
473	1384			
474	1385			
475	1386	2180	2836	787_8454
476	1387	2181	2837	790_8424
477	1388			
478	1389	2182	2838	787_9580
479	1390	2183	2839	784_6906
480	1391	2184	2840	787_1411
481	1392	2185	2841	790_10999
482	1393			
483	1394			
484	1395			
485	1396			
486	1397	2186	2842	787_2916
487	1398	2187	2843	787_5986
488	1399	2188	2844	785_2979
489	1400	2189	2845	785_2105
490	1401			
491	1402			
492	1403	2190	2846	785_3046
493	1404	2191	2847	788_9546
494	1405	2192	2848	785_2158
495	1406			
496	1407	2193	2849	784_7549
497	1408	2194	2850	784_1066
498	1409	2195	2851	784_2673
499	1410	2196	2852	785_563
500	1411			
501	1412	2197	2853	789_630
502	1413	2198	2854	785_259
503	1414	2199	2855	784_5637
504	1415	2200	2856	790_7396
505	1416			
506	1417	2201	2857	790_11548
507	1418			
508	1419	2202	2858	784_6740
509	1420			
510	1421	2203	2859	785_1007

Table 9
1145

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
511	1422			
512	1423			
513	1424	2204	2860	784_3641
514	1425			
515	1426	2205	2861	789_6066
516	1427	2206	2862	788_13582
517	1428	2207	2863	784_9762
518	1429	2208	2864	787_2052
519	1430	2209	2865	790_3055
520	1431			
521	1432	2210	2866	790_23800
522	1433	2211	2867	790_23800
523	1434			
524	1435	2212	2868	787_2548
525	1436			
526	1437	2213	2869	784_2565
527	1438	2214	2870	784_544
528	1439	2215	2871	784_544
529	1440			
530	1441	2216	2872	789_1844
531	1442	2217	2873	787_2733
532	1443	2218	2874	785_493
533	1444	2219	2875	790_18203
534	1445			
535	1446	2220	2876	784_3336
536	1447	2221	2877	790_777
537	1448	2222	2878	787_4220
538	1449	2223	2879	790_26438
539	1450	2224	2880	790_13586
540	1451	2225	2881	784_270
541	1452			
542	1453	2226	2882	790_14176
543	1454	2227	2883	784_3543
544	1455	2228	2884	784_3575
545	1456	2229	2885	787_5638
546	1457	2230	2886	784_3826
547	1458	2231	2887	787_6059
548	1459	2232	2888	787_2585
549	1460			
550	1461			
551	1462	2233	2889	787_2965
552	1463			
553	1464	2234	2890	790_13050
554	1465			
555	1466	2235	2891	784_3374
556	1467	2236	2892	787_8240
557	1468	2237	2893	784_4398
558	1469			
559	1470	2238	2894	788_10891
560	1471	2239	2895	787_9805
561	1472			

Table 9
1146

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
562	1473			
563	1474	2240	2896	787_7094
564	1475	2241	2897	787_5209
565	1476	2242	2898	784_582
566	1477	2243	2899	790_10111
567	1478	2244	2900	790_13563
568	1479			
569	1480	2245	2901	787_8234
570	1481			
571	1482	2246	2902	790_16394
572	1483			
573	1484	2247	2903	790_18452
574	1485	2248	2904	790_211
575	1486	2249	2905	790_14932
576	1487			
577	1488	2250	2906	787_7498
578	1489	2251	2907	787_610
579	1490	2252	2908	790_19096
580	1491	2253	2909	784_7363
581	1492	2254	2910	792_8355
582	1493	2255	2911	787_1179
583	1494	2256	2912	790_6822
584	1495	2257	2913	784_8670
585	1496	2258	2914	784_2469
586	1497			
587	1498	2259	2915	790_15720
588	1499	2260	2916	790_11300
589	1500	2261	2917	784_190
590	1501			
591	1502	2262	2918	789_6245
592	1503	2263	2919	787_7385
593	1504	2264	2920	790_281
594	1505	2265	2921	784_6192
595	1506	2266	2922	790_770
596	1507	2267	2923	784_3364
597	1508	2268	2924	784_5424
598	1509			
599	1510	2269	2925	790_10118
600	1511			
601	1512			
602	1513	2270	2926	785_2555
603	1514			
604	1515			
605	1516	2271	2927	790_20185
606	1517	2272	2928	784_333
607	1518	2273	2929	792_3164
608	1519			
609	1520			
610	1521	2274	2930	784_3455
611	1522	2275	2931	784_506
612	1523	2276	2932	788_7179

Table 9
1147

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
613	1524			
614	1525			
615	1526	2277	2933	790_13445
616	1527			
617	1528	2278	2934	784_6181
618	1529	2279	2935	784_4453
619	1530			
620	1531	2280	2936	784_8140
621	1532			
622	1533	2281	2937	784_3441
623	1534	2282	2938	787_6194
624	1535	2283	2939	784_1407
625	1536			
626	1537	2284	2940	790_8886
627	1538			
628	1539	2285	2941	785_2555
629	1540	2286	2942	784_688
630	1541	2287	2943	784_8302
631	1542	2288	2944	787_2581
632	1543	2289	2945	790_19616
633	1544	2290	2946	784_4663
634	1545	2291	2947	790_9138
635	1546			
636	1547	2292	2948	784_4743
637	1548	2293	2949	790_12541
638	1549			
639	1550			
640	1551	2294	2950	784_4128
641	1552			
642	1553	2295	2951	790_19867
643	1554	2296	2952	784_7061
644	1555	2297	2953	785_1399
645	1556	2298	2954	784_5565
646	1557	2299	2955	790_10780
647	1558			
648	1559			
649	1560	2300	2956	784_2148
650	1561	2301	2957	790_24174
651	1562	2302	2958	784_4307
652	1563	2303	2959	790_20063
653	1564			
654	1565	2304	2960	784_7654
655	1566	2305	2961	784_7454
656	1567	2306	2962	790_8324
657	1568	2307	2963	784_5860
658	1569			
659	1570	2308	2964	788_11718
660	1571	2309	2965	784_2105
661	1572			
662	1573	2310	2966	785_1924
663	1574	2311	2967	784_8098

Table 9
1148

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
664	1575	2312	2968	784_2320
665	1576	2313	2969	784_7695
666	1577	2314	2970	784_6847
667	1578			
668	1579			
669	1580	2315	2971	784_8098
670	1581	2316	2972	784_4781
671	1582			
672	1583	2317	2973	792_8335
673	1584			
674	1585	2318	2974	789_2488
675	1586	2319	2975	785_2433
676	1587			
677	1588	2320	2976	787_3115
678	1589			
679	1590	2321	2977	787_5209
680	1591	2322	2978	787_4223
681	1592	2323	2979	784_5228
682	1593	2324	2980	787_5094
683	1594	2325	2981	790_10116
684	1595			
685	1596	2326	2982	785_1351
686	1597			
687	1598			
688	1599	2327	2983	784_4288
689	1600	2328	2984	784_4816
690	1601	2329	2985	791_3535
691	1602	2330	2986	784_4322
692	1603	2331	2987	785_2272
693	1604	2332	2988	790_12959
694	1605	2333	2989	784_4642
695	1606	2334	2990	784_3534
696	1607			
697	1608			
698	1609			
699	1610	2335	2991	784_2904
700	1611	2336	2992	784_8547
701	1612			
702	1613			
703	1614	2337	2993	785_2907
704	1615			
705	1616	2338	2994	789_3856
706	1617	2339	2995	785_2043
707	1618	2340	2996	784_4327
708	1619	2341	2997	787_10225
709	1620			
710	1621	2342	2998	790_24136
711	1622	2343	2999	785_172
712	1623	2344	3000	790_24958
713	1624	2345	3001	790_17848
714	1625	2346	3002	790_10920

Table 9
1149

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
715	1626	2347	3003	790_24477
716	1627	2348	3004	790_21024
717	1628	2349	3005	790_3053
718	1629			
719	1630	2350	3006	790_13392
720	1631	2351	3007	790_28822
721	1632	2352	3008	790_17805
722	1633	2353	3009	784_1991
723	1634	2354	3010	790_12778
724	1635	2355	3011	784_5899
725	1636			
726	1637	2356	3012	784_4851
727	1638	2357	3013	784_6070
728	1639	2358	3014	784_9615
729	1640	2359	3015	790_23719
730	1641			
731	1642	2360	3016	784_7918
732	1643	2361	3017	790_16176
733	1644			
734	1645	2362	3018	784_4042
735	1646			
736	1647	2363	3019	790_4484
737	1648			
738	1649	2364	3020	790_16690
739	1650	2365	3021	784_7703
740	1651	2366	3022	785_2626
741	1652			
742	1653	2367	3023	784_1423
743	1654			
744	1655			
745	1656	2368	3024	784_8178
746	1657	2369	3025	784_6726
747	1658	2370	3026	792_7162
748	1659	2371	3027	784_2948
749	1660			
750	1661	2372	3028	784_2988
751	1662			
752	1663	2373	3029	784_10047
753	1664			
754	1665	2374	3030	787_3415
755	1666			
756	1667	2375	3031	787_10007
757	1668			
758	1669			
759	1670	2376	3032	790_12779
760	1671			
761	1672	2377	3033	785_3699
762	1673	2378	3034	784_4026
763	1674	2379	3035	790_14323
764	1675			
765	1676			

Table 9
1150

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
766	1677	2380	3036	792_2616
767	1678	2381	3037	787_6570
768	1679	2382	3038	784_2590
769	1680	2383	3039	784_5216
770	1681			
771	1682	2384	3040	790_12514
772	1683			
773	1684			
774	1685	2385	3041	785_3366
775	1686	2386	3042	790_12446
776	1687			
777	1688			
778	1689			
779	1690			
780	1691	2387	3043	784_6708
781	1692	2388	3044	784_852
782	1693			
783	1694			
784	1695			
785	1696	2389	3045	784_9460
786	1697	2390	3046	787_7895
787	1698	2391	3047	784_6226
788	1699	2392	3048	789_5263
789	1700	2393	3049	784_4933
790	1701			
791	1702			
792	1703			
793	1704	2394	3050	784_7176
794	1705			
795	1706	2395	3051	784_3074
796	1707			
797	1708	2396	3052	785_1642
798	1709			
799	1710	2397	3053	790_12671
800	1711			
801	1712			
802	1713	2398	3054	784_1127
803	1714			
804	1715			
805	1716	2399	3055	790_14423
806	1717	2400	3056	790_28166
807	1718			
808	1719			
809	1720	2401	3057	784_5946
810	1721	2402	3058	784_4850
811	1722	2403	3059	784_744
812	1723	2404	3060	790_13151
813	1724			
814	1725	2405	3061	787_7172
815	1726	2406	3062	790_6384
816	1727			

Table 9
1151

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
817	1728			
818	1729	2407	3063	785_3645
819	1730	2408	3064	784_9630
820	1731			
821	1732	2409	3065	784_10027
822	1733	2410	3066	784_10083
823	1734	2411	3067	787_2031
824	1735	2412	3068	784_4592
825	1736			
826	1737	2413	3069	790_3308
827	1738			
828	1739	2414	3070	784_4360
829	1740	2415	3071	785_2472
830	1741	2416	3072	784_2060
831	1742	2417	3073	784_3549
832	1743			
833	1744	2418	3074	784_1872
834	1745	2419	3075	784_7925
835	1746	2420	3076	784_5564
836	1747			
837	1748			
838	1749	2421	3077	785_1472
839	1750	2422	3078	784_2232
840	1751	2423	3079	790_24132
841	1752	2424	3080	790_6689
842	1753	2425	3081	787_3699
843	1754	2426	3082	785_2955
844	1755	2427	3083	784_4324
845	1756	2428	3084	784_9382
846	1757	2429	3085	787_7087
847	1758			
848	1759	2430	3086	784_4912
849	1760			
850	1761	2431	3087	790_17236
851	1762	2432	3088	790_1914
852	1763	2433	3089	784_466
853	1764	2434	3090	790_11164
854	1765			
855	1766	2435	3091	787_8100
856	1767	2436	3092	784_9062
857	1768			
858	1769	2437	3093	784_4141
859	1770			
860	1771	2438	3094	784_1365
861	1772	2439	3095	784_6642
862	1773			
863	1774	2440	3096	789_3442
864	1775	2441	3097	784_10198
865	1776	2442	3098	790_11264
866	1777			
867	1778	2443	3099	788_13640

Table 9
1152

SEQ ID NO: of full-length nucleotide sequence	SEQ ID NO: of full-length peptide sequence	SEQ ID NO: of contig nucleotide sequence	SEQ ID NO: of contig peptide sequence	Identification of Priority Application that contig nucleotide sequence was filed (Attorney Docket No._SEQ ID NO.) *
868	1779			
869	1780	2444	3100	785_238
870	1781	2445	3101	787_10243
871	1782	2446	3102	784_8555
872	1783	2447	3103	789_5245
873	1784	2448	3104	784_4968
874	1785	2449	3105	789_5631
875	1786	2450	3106	784_6373
876	1787	2451	3107	784_7992
877	1788	2452	3108	787_6002
878	1789	2453	3109	784_1503
879	1790	2454	3110	790_10504
880	1791	2455	3111	790_18438
881	1792	2456	3112	790_13790
882	1793	2457	3113	790_21890
883	1794	2458	3114	790_17754
884	1795			
885	1796	2459	3115	785_1016
886	1797	2460	3116	785_14
887	1798	2461	3117	790_18472
888	1799	2462	3118	784_8233
889	1800	2463	3119	784_177
890	1801	2464	3120	784_3522
891	1802	2465	3121	784_10067
892	1803	2466	3122	784_7868
893	1804			
894	1805	2467	3123	787_7085
895	1806	2468	3124	784_3739
896	1807	2469	3125	784_4168
897	1808	2470	3126	784_6642
898	1809			
899	1810	2471	3127	789_6290
900	1811	2472	3128	791_2423
901	1812			
902	1813			
903	1814			
904	1815			
905	1816	2473	3129	790_10106
906	1817	2474	3130	787_3075
907	1818	2475	3131	790_17762
908	1819	2476	3132	784_482
909	1820	2477	3133	790_21059
910	1821	2478	3134	788_13847
911	1822			

*784_XXX = SEQ ID NO: XXX of Attorney Docket No. 784, US Serial No. 09/488,725 filed 01/21/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

Table 9

1153

785_XXX = SEQ ID NO: XXX of Attorney Docket No. 785, US Serial No. 09/491,404 filed 01/25/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

787_XXX = SEQ ID NO: XXX of Attorney Docket No. 787, US Serial No. 09/496,914 filed 02/03/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

788_XXX = SEQ ID NO: XXX of Attorney Docket No. 788, US Serial No. 09/515,126 filed 02/28/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

789_XXX = SEQ ID NO: XXX of Attorney Docket No. 789, US Serial No. 09/519,705 filed 03/07/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

790_XXX = SEQ ID NO: XXX of Attorney Docket No. 790, US Serial No. 09/540,217 filed 03/31/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

791_XXX = SEQ ID NO: XXX of Attorney Docket No. 791, US Serial No. 09/552,929 filed 04/18/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

792_XXX = SEQ ID NO: XXX of Attorney Docket No. 792, US Serial No. 09/577,408 filed 05/18/2000, the entire disclosure of which, including sequence listing, is incorporated herein by reference.

Table 10
1154

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/339,739
1	912	1
2	913	2
3	914	3
4	915	4
5	916	5
6	917	6
7	918	7
8	919	8
9	920	9
10	921	10
11	922	11
12	923	12
13	924	13
14	925	14
15	926	15
16	927	16
17	928	17
18	929	18
19	930	19
20	931	20
21	932	21
22	933	22
23	934	23
24	935	24
25	936	25
26	937	26
27	938	27
28	939	28
29	940	29
30	941	30
31	942	31
32	943	32
33	944	33
34	945	34
35	946	35
36	947	36
37	948	37
38	949	38
39	950	39
40	951	40
41	952	41
42	953	42
43	954	43
44	955	44
45	956	45
46	957	46
47	958	47
48	959	48
49	960	49
50	961	50
51	962	51
52	963	52

Table 10

1155

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/339,739
53	964	53
54	965	54
55	966	55
56	967	56
57	968	57
58	969	58
59	970	59
60	971	60
61	972	61
62	973	62
63	974	63
64	975	64
65	976	65
66	977	66
67	978	67
68	979	68
69	980	69
70	981	70
71	982	71
72	983	72
73	984	73
74	985	74
75	986	75
76	987	76
77	988	77
78	989	78
79	990	79
80	991	80
81	992	81
82	993	82
83	994	83
84	995	84
85	996	85
86	997	86
87	998	87
88	999	88
89	1000	89
90	1001	90
91	1002	91
92	1003	92
93	1004	93
94	1005	94
95	1006	95
96	1007	96
97	1008	97
98	1009	98
99	1010	99
100	1011	100
101	1012	101
102	1013	102
103	1014	103
104	1015	104

Table 10

1156

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/339,739
105	1016	105
106	1017	106
107	1018	107
108	1019	108
109	1020	109
110	1021	110
111	1022	111
112	1023	112
113	1024	113
114	1025	114
115	1026	115
116	1027	116
117	1028	117
118	1029	118
119	1030	119
120	1031	120
121	1032	121
122	1033	122
123	1034	123
124	1035	124
125	1036	125

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/339,453
126	1037	1
127	1038	2
128	1039	3
129	1040	4
130	1041	5
131	1042	7
132	1043	8
133	1044	9
134	1045	10
135	1046	11
136	1047	12
137	1048	13
138	1049	14
139	1050	15
140	1051	16
141	1052	17
142	1053	18
143	1054	19
144	1055	20
145	1056	21
146	1057	22
147	1058	23
148	1059	24
149	1060	25
150	1061	26
151	1062	27

Table 10
1157

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/339,453
152	1063	28
153	1064	29
154	1065	30
155	1066	31
156	1067	32
157	1068	33
158	1069	34
159	1070	35
160	1071	36
161	1072	37
162	1073	38
163	1074	39
164	1075	40
165	1076	41
166	1077	42
167	1078	43
168	1079	44
169	1080	45
170	1081	46
171	1082	47
172	1083	48
173	1084	49
174	1085	50
175	1086	51
176	1087	52
177	1088	53
178	1089	54
179	1090	55
180	1091	56
181	1092	57
182	1093	58
183	1094	59
184	1095	60
185	1096	61
186	1097	62
187	1098	63
188	1099	64
189	1100	65
190	1101	66
191	1102	67
192	1103	68
193	1104	69
194	1105	70
195	1106	71
196	1107	72
197	1108	73
198	1109	74
199	1110	75
200	1111	76
201	1112	77
202	1113	78
203	1114	79

Table 10

1158

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/339,453
204	1115	80
205	1116	81
206	1117	82
207	1118	83
208	1119	84
209	1120	85
210	1121	86
211	1122	87
212	1123	88
213	1124	89
214	1125	90
215	1126	91
216	1127	92
217	1128	93
218	1129	94
219	1130	95
220	1131	96
221	1132	97
222	1133	98
223	1134	99
224	1135	100
225	1136	101
226	1137	102
227	1138	103
228	1139	104
229	1140	105
230	1141	106
231	1142	107
232	1143	108
233	1144	109
234	1145	110
235	1146	111
236	1147	112
237	1148	113
238	1149	114
239	1150	115
240	1151	116
241	1152	117
242	1153	118
243	1154	119
244	1155	120
245	1156	121
246	1157	122
247	1158	123
248	1159	124

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,384
249	1160	3
250	1161	4

Table 10

1159

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,384
251	1162	5
252	1163	6
253	1164	8
254	1165	12
255	1166	14
256	1167	15
257	1168	17
258	1169	18
259	1170	19
260	1171	20
261	1172	21
262	1173	22
263	1174	23
264	1175	24
265	1176	25
266	1177	26
267	1178	27
268	1179	28
269	1180	29
270	1181	30
271	1182	31
272	1183	32
273	1184	33
274	1185	34
275	1186	35
276	1187	36
277	1188	37
278	1189	38
279	1190	39
280	1191	40
281	1192	41
282	1193	42
283	1194	43
284	1195	44
285	1196	45
286	1197	46
287	1198	47
288	1199	48
289	1200	49
290	1201	50
291	1202	51
292	1203	52
293	1204	53
294	1205	54
295	1206	55
296	1207	56
297	1208	57
298	1209	58
299	1210	59
300	1211	60
301	1212	61
302	1213	62

Table 10

1160

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,384
303	1214	63
304	1215	64
305	1216	65
306	1217	66
307	1218	67
308	1219	68
309	1220	69
310	1221	70
311	1222	71
312	1223	72
313	1224	73
314	1225	74
315	1226	75
316	1227	76
317	1228	77
318	1229	78
319	1230	79
320	1231	80
321	1232	81
322	1233	82
323	1234	83
324	1235	84
325	1236	85
326	1237	86
327	1238	87
328	1239	88
329	1240	89
330	1241	90
331	1242	91
332	1243	92
333	1244	93
334	1245	94
335	1246	95
336	1247	96
337	1248	97
338	1249	98
339	1250	99
340	1251	100
341	1252	101
342	1253	102
343	1254	103
344	1255	104
345	1256	105
346	1257	106
347	1258	107
348	1259	108
349	1260	109
350	1261	110
351	1262	111
352	1263	112
353	1264	113
354	1265	114

Table 10

1161

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,384
355	1266	115
356	1267	116
357	1268	117
358	1269	118
359	1270	119
360	1271	120
361	1272	121
362	1273	122
363	1274	123
364	1275	124
365	1276	125
366	1277	126
367	1278	127
368	1279	128
369	1280	129
370	1281	130
371	1282	131
372	1283	132
373	1284	133
374	1285	134
375	1286	135
376	1287	136
377	1288	137
378	1289	138
379	1290	139
380	1291	140
381	1292	141
382	1293	142
383	1294	143
384	1295	144
385	1296	145
386	1297	146
387	1298	147
388	1299	148
389	1300	149
390	1301	150
391	1302	151
392	1303	152
393	1304	153
394	1305	154
395	1306	155
396	1307	156
397	1308	157
398	1309	158
399	1310	159
400	1311	160
401	1312	161
402	1313	162
403	1314	163
404	1315	164
405	1316	165
406	1317	166

Table 10

1162

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,384
407	1318	167
408	1319	169
409	1320	170
410	1321	171
411	1322	172
412	1323	173
413	1324	174
414	1325	175
415	1326	176
416	1327	177
417	1328	178
418	1329	179

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,091
419	1330	2
420	1331	4
421	1332	5
422	1333	6
423	1334	8
424	1335	9
425	1336	10
426	1337	11
427	1338	12
428	1339	14
429	1340	15
430	1341	16
431	1342	17
432	1343	18
433	1344	19
434	1345	20
435	1346	21
436	1347	22
437	1348	24
438	1349	25
439	1350	26
440	1351	27
441	1352	28
442	1353	29
443	1354	32
444	1355	33
445	1356	34
446	1357	35
447	1358	36
448	1359	37
449	1360	38
450	1361	39
451	1362	40
452	1363	41
453	1364	42

Table 10

1163

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,091
454	1365	43
455	1366	44
456	1367	45
457	1368	46
458	1369	47
459	1370	48
460	1371	49
461	1372	50
462	1373	51
463	1374	52
464	1375	53
465	1376	54
466	1377	55
467	1378	56
468	1379	57
469	1380	58
470	1381	59
471	1382	60
472	1383	61
473	1384	62
474	1385	63
475	1386	64
476	1387	65
477	1388	66
478	1389	67
479	1390	68
480	1391	69
481	1392	70
482	1393	71
483	1394	72
484	1395	73
485	1396	74
486	1397	75
487	1398	76
488	1399	77
489	1400	78
490	1401	79
491	1402	80
492	1403	81
493	1404	82
494	1405	83
495	1406	84
496	1407	85
497	1408	86
498	1409	87
499	1410	88
500	1411	89
501	1412	90
502	1413	91
503	1414	92
504	1415	93
505	1416	94

Table 10
1164

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/365,091
506	1417	95
507	1418	96
508	1419	97
509	1420	98
510	1421	99
511	1422	100
512	1423	101
513	1424	102
514	1425	103
515	1426	104
516	1427	105
517	1428	106
518	1429	107
519	1430	108
520	1431	109
521	1432	110
522	1433	111
523	1434	112
524	1435	113
525	1436	114
526	1437	115
527	1438	116
528	1439	117
529	1440	118
530	1441	119
531	1442	120
532	1443	121
533	1444	122
534	1445	123
535	1446	124
536	1447	125
537	1448	126
538	1449	127
539	1450	128
540	1451	129
541	1452	130
542	1453	131
543	1454	132
544	1455	133
545	1456	135
546	1457	136
547	1458	137
548	1459	138
549	1460	139
550	1461	140
551	1462	141
552	1463	142
553	1464	143
554	1465	144
555	1466	145

Table 10

1165

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,615
556	1467	2
557	1468	3
558	1469	4
559	1470	5
560	1471	6
561	1472	7
562	1473	8
563	1474	9
564	1475	10
565	1476	11
566	1477	12
567	1478	13
568	1479	14
569	1480	15
570	1481	16
571	1482	17
572	1483	18
573	1484	19
574	1485	20
575	1486	21
576	1487	22
577	1488	23
578	1489	24
579	1490	25
580	1491	26
581	1492	27
582	1493	28
583	1494	29
584	1495	30
585	1496	31
586	1497	32
587	1498	33
588	1499	34
589	1500	35
590	1501	36
591	1502	37
592	1503	38
593	1504	39
594	1505	40
595	1506	41
596	1507	42
597	1508	43
598	1509	44
599	1510	45
600	1511	46
601	1512	47
602	1513	48
603	1514	49
604	1515	50
605	1516	51
606	1517	52
607	1518	53

Table 10
1166

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,615
608	1519	54
609	1520	55
610	1521	56
611	1522	57
612	1523	58
613	1524	59
614	1525	60
615	1526	61
616	1527	62
617	1528	63
618	1529	64
619	1530	65
620	1531	66
621	1532	67
622	1533	68
623	1534	69
624	1535	70
625	1536	71
626	1537	72
627	1538	73
628	1539	74
629	1540	75
630	1541	76
631	1542	77
632	1543	78
633	1544	79
634	1545	80
635	1546	81
636	1547	82
637	1548	83
638	1549	84
639	1550	85
640	1551	86
641	1552	87
642	1553	88
643	1554	89
644	1555	90
645	1556	91
646	1557	92
647	1558	93
648	1559	94
649	1560	95
650	1561	96
651	1562	97
652	1563	98
653	1564	99
654	1565	100
655	1566	101
656	1567	102
657	1568	103
658	1569	104
659	1570	105

Table 10

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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,615
660	1571	106
661	1572	107
662	1573	108
663	1574	109
664	1575	110
665	1576	111
666	1577	112
667	1578	113
668	1579	114
669	1580	115
670	1581	116
671	1582	117
672	1583	118
673	1584	119
674	1585	120
675	1586	121
676	1587	122
677	1588	123
678	1589	124
679	1590	125
680	1591	126
681	1592	127
682	1593	128
683	1594	129
684	1595	130
685	1596	131
686	1597	132
687	1598	133
688	1599	134
689	1600	135
690	1601	136
691	1602	137
692	1603	138
693	1604	139
694	1605	140
695	1606	141
696	1607	142
697	1608	143
698	1609	144
699	1610	145
700	1611	146
701	1612	147
702	1613	148
703	1614	149
704	1615	150
705	1616	151
706	1617	152
707	1618	153
708	1619	154
709	1620	155
710	1621	157
711	1622	158

Table 10
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,615
712	1623	159
713	1624	160
714	1625	161
715	1626	162
716	1627	163
717	1628	164
718	1629	165
719	1630	166
720	1631	167
721	1632	168
722	1633	169
723	1634	170
724	1635	171
725	1636	172
726	1637	173
727	1638	174
728	1639	175
729	1640	176
730	1641	177
731	1642	178
732	1643	179
733	1644	180
734	1645	181
735	1646	182
736	1647	183
737	1648	184
738	1649	185
739	1650	186
740	1651	187
741	1652	188
742	1653	189
743	1654	190
744	1655	191
745	1656	192
746	1657	193
747	1658	194
748	1659	195
749	1660	196
750	1661	197
751	1662	198
752	1663	199
753	1664	200
754	1665	201
755	1666	202
756	1667	203
757	1668	204
758	1669	205
759	1670	206
760	1671	207
761	1672	208
762	1673	209
763	1674	210

Table 10

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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,615
764	1675	211
765	1676	212
766	1677	213
767	1678	214
768	1679	215
769	1680	216
770	1681	217
771	1682	218
772	1683	219
773	1684	220
774	1685	221
775	1686	222
776	1687	223
777	1688	224
778	1689	225
779	1690	226
780	1691	227
781	1692	228
782	1693	229
783	1694	230
784	1695	231
785	1696	233
786	1697	234
787	1698	235
788	1699	236
789	1700	237
790	1701	238
791	1702	239
792	1703	240
793	1704	241
794	1705	242
795	1706	243
796	1707	244
797	1708	245
798	1709	246
799	1710	247
800	1711	248
801	1712	249
802	1713	250
803	1714	251
804	1715	252
805	1716	253
806	1717	254
807	1718	255
808	1719	256

SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,381
809	1720	1
810	1721	2

Table 10
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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,381
811	1722	3
812	1723	4
813	1724	5
814	1725	6
815	1726	7
816	1727	8
817	1728	9
818	1729	10
819	1730	11
820	1731	12
821	1732	13
822	1733	14
823	1734	15
824	1735	16
825	1736	17
826	1737	18
827	1738	19
828	1739	20
829	1740	21
830	1741	22
831	1742	23
832	1743	24
833	1744	25
834	1745	26
835	1746	27
836	1747	28
837	1748	29
838	1749	30
839	1750	31
840	1751	32
841	1752	33
842	1753	34
843	1754	35
844	1755	36
845	1756	37
846	1757	38
847	1758	39
848	1759	40
849	1760	41
850	1761	42
851	1762	43
852	1763	44
853	1764	45
854	1765	46
855	1766	47
856	1767	48
857	1768	49
858	1769	50
859	1770	51
860	1771	52
861	1772	53
862	1773	54

Table 10

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SEQ ID NO of Full-length Nucleotide Sequence	SEQ ID NO of Full-length Peptide Sequence	SEQ ID NO in Priority Application USSN 60/372,381
863	1774	55
864	1775	56
865	1776	57
866	1777	58
867	1778	59
868	1779	60
869	1780	61
870	1781	62
871	1782	63
872	1783	64
873	1784	65
874	1785	66
875	1786	67
876	1787	68
877	1788	69
878	1789	70
879	1790	71
880	1791	72
881	1792	73
882	1793	74
883	1794	75
884	1795	76
885	1796	77
886	1797	78
887	1798	79
888	1799	80
889	1800	81
890	1801	82
891	1802	83
892	1803	84
893	1804	85
894	1805	86
895	1806	87
896	1807	88
897	1808	89
898	1809	90
899	1810	91
900	1811	92
901	1812	93
902	1813	94
903	1814	95
904	1815	96
905	1816	97
906	1817	98
907	1818	99
908	1819	100
909	1820	101
910	1821	102
911	1822	103

WHAT IS CLAIMED IS:

1. An isolated polynucleotide comprising a nucleotide sequence selected from the group consisting of SEQ ID NO: 1-911.

2. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide hybridizes to the polynucleotide of claim 1 under stringent hybridization conditions.

3. An isolated polynucleotide encoding a polypeptide with biological activity, wherein said polynucleotide has greater than about 99% sequence identity with the polynucleotide of claim 1.

4. The polynucleotide of claim 1 wherein said polynucleotide is DNA.

5. An isolated polynucleotide of claim 1 wherein said polynucleotide comprises the complementary sequences.

6. A vector comprising the polynucleotide of claim 1.

7. An expression vector comprising the polynucleotide of claim 1.

8. A host cell genetically engineered to comprise the polynucleotide of claim 1.

9. A host cell genetically engineered to comprise the polynucleotide of claim 1 operatively associated with a regulatory sequence that modulates expression of the polynucleotide in the host cell.

10. An isolated polypeptide, wherein the polypeptide is selected from the group consisting of:

(a) a polypeptide encoded by any one of the polynucleotides of claim 1; and

(b) a polypeptide encoded by a polynucleotide hybridizing under stringent conditions with any one of SEQ ID NO: 1-911.

11. A composition comprising the polypeptide of claim 10 and a carrier.

12. An antibody directed against the polypeptide of claim 10.

13. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polynucleotide of claim 1 for a period sufficient to form the complex; and

b) detecting the complex, so that if a complex is detected, the polynucleotide of claim 1 is detected.

14. A method for detecting the polynucleotide of claim 1 in a sample, comprising:

a) contacting the sample under stringent hybridization conditions with nucleic acid primers that anneal to the polynucleotide of claim 1 under such conditions;

b) amplifying a product comprising at least a portion of the polynucleotide of claim 1; and

c) detecting said product and thereby the polynucleotide of claim 1 in the sample.

15. The method of claim 14, wherein the polynucleotide is an RNA molecule and the method further comprises reverse transcribing an annealed RNA molecule into a cDNA polynucleotide.

16. A method for detecting the polypeptide of claim 10 in a sample, comprising:

a) contacting the sample with a compound that binds to and forms a complex with the polypeptide under conditions and for a period sufficient to form the complex; and

b) detecting formation of the complex, so that if a complex formation is detected, the polypeptide of claim 10 is detected.

17. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10 under conditions sufficient to form a polypeptide/compound complex; and

b) detecting the complex, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

18. A method for identifying a compound that binds to the polypeptide of claim 10, comprising:

a) contacting the compound with the polypeptide of claim 10, in a cell, under conditions sufficient to form a polypeptide/compound complex, wherein the complex drives expression of a reporter gene sequence in the cell; and

b) detecting the complex by detecting reporter gene sequence expression, so that if the polypeptide/compound complex is detected, a compound that binds to the polypeptide of claim 10 is identified.

19. A method of producing the polypeptide of claim 10, comprising,

a) culturing a host cell comprising a polynucleotide sequence selected from the group consisting of any of the polynucleotides from SEQ ID NO: 1-911, under conditions sufficient to express the polypeptide in said cell; and

b) isolating the polypeptide from the cell culture or cells of step (a).

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of any one of the polypeptides SEQ ID NO: 912-1822.

21. The polypeptide of claim 20 wherein the polypeptide is provided on a polypeptide array.

22. A collection of polynucleotides, wherein the collection comprising of at least one of SEQ ID NO: 1-911.

23. The collection of claim 22, wherein the collection is provided on a nucleic acid array.

24. The collection of claim 23, wherein the array detects full-matches to any one of the polynucleotides in the collection.

25. The collection of claim 23, wherein the array detects mismatches to any one of the polynucleotides in the collection.

26. The collection of claim 22, wherein the collection is provided in a computer-readable format.

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(54) Title: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES

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A. CLASSIFICATION OF SUBJECT MATTER

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Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)
Compugen, SEQ ID NO: 1

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	VOLLRATH, D. et al, The human Y chromosome: A 43-interval map based on naturally occurring deletions, Science, 2 October 1992, Vol. 258, pages 52-59, see entire document.	1-9, 13-15, 19, and 22-26

☐ Further documents are listed in the continuation of Box C. ☐ See patent family annex.

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